



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142047

To: Jeffrey Parkin
Location: rem/3d39/3c18
Art Unit: 1648
Friday, January 21, 2005

Case Serial Number: 10/085944

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

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From: 72607
Sent: Parkin, Jeffrey
Friday, January 07, 2005 9:05 PM
To: STIC-Biotech/ChemLib
Subject: Sequence Search for U.S. Serial No. 10/085,944

Would you please search **SEQ ID NO.: 2** from the aforementioned application (U.S. Serial No. 10/085,944; Wang, W.) v. all relevant **PUBLIC/COMMERCIAL** databases.

Place results on **PAPER**.

Please include the first **50 SUMMARIES**.

Thanks!

JSP
AU 1648
REM 3D39
2-0908

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors:

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
✓ Other CEN

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result	No.	Score	Query	Length	DB	ID	Description
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3	3	28	100.0	840	14	AF360861	Dengue vi
4	4	28	100.0	840	14	AF360862	Dengue vi
5	5	28	100.0	840	14	AF360863	Dengue vi
6	6	28	100.0	2319	14	S66064	structural
7	7	28	100.0	2325	14	AF469175	Dengue vi
8	8	28	100.0	2325	14	AF469176	Dengue vi
9	9	28	100.0	2325	14	AF509530	Dengue vi
10	10	28	100.0	2325	14	AY044442	Dengue vi
11	11	28	100.0	2357	6	AR232496	Sequence
12	12	28	100.0	2357	14	DEN2NGC	D00346 Dengue viru
13	13	28	100.0	2469	14	DEN2TAM	M15075 Dengue viru
14	14	28	100.0	2552	14	AY152036S1	Dengue vi
15	15	28	100.0	2552	14	AY152040S1	Dengue vi
16	16	28	100.0	2552	14	AY152044S1	Dengue vi
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18	18	28	100.0	2552	14	AY152052S1	Dengue vi
19	19	28	100.0	2552	14	AY152056S1	Dengue vi

TITLE	Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for in situ virus evolution and recombination
JOURNAL	J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
MEDLINE	21571640
PUBMED	11714970
REFERENCE	2 (bases 1 to 840)
AUTHORS	Uzcategui,N.Y., Canacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,E.C. and Gould,E.A.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road, Oxford OX2 6UD, England
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Db	40 AATATGCTGAACCGGAGAGAAACCGCG 67
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DEFINITION	Dengue virus type 2 isolate LARD1996 polyprotein gene, partial cds.
ACCESSION	AF360863
VERSION	AF360863.1 GI:18644127
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SOURCE	Dengue virus type 2
ORGANISM	Dengue virus type 2
	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
REFERENCE	1 (bases 1 to 840)
AUTHORS	Uzcategui,N.Y., Canacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,E.C. and Gould,E.A.
TITLE	Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for in situ virus evolution and recombination
JOURNAL	J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
MEDLINE	21571640
PUBMED	11714970
REFERENCE	2 (bases 1 to 840)
AUTHORS	Uzcategui,N.Y., Canacho,D., Comach,G., Cuello de Uzcategui,R., Holmes,E.C. and Gould,E.A.
TITLE	Direct Submission
JOURNAL	Submitted (15-MAR-2001) Flavivirus, CEH-Oxford, Mansfield Road, Oxford OX2 6UD, England
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LOCUS	S66064	2319 bp DNA linear VRL 04-DEC-1993
DEFINITION	structural polyprotein [dengue type 4 virus DEN4, H241-P, Genomic, 2319 nt].	
ACCESSION	S66064	
VERSION	S66064.1	GI:432575
KEYWORDS	Dengue virus type 4	
SOURCE	Dengue virus type 4	
ORGANISM	Viruses; SERNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	
REFERENCE	1 (bases 1 to 2319)	
AUTHORS	Kawano, H., Rostaphov, V., Rosen, L. and Lai, C.J.	
TITLE	Genetic determinants of dengue type 4 virus neurovirulence for mice	
JOURNAL	J. Virol. 67 (11), 6567-6575 (1993)	
MEDLINE	94016840	
PUBMED	8411360	
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 138430] from the original journal article.	
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gene	1. .2319	
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DEFINITION	Dengue virus type 2 strain GD24/93 polyprotein gene, partial cds.				
ACCESSION	AF469175				
VERSION	AF469175.1				
KEYWORDS	GI:18766554				
SOURCE	Dengue virus type 2				
ORGANISM	Dengue virus type 2				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.				
AUTHORS	1 (bases 1 to 2325)				
TITLE	Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and Zhao,W.Z.				
JOURNAL	Structural genes of dengue virus type 2 strain GD24/93 isolate from Nanhai, Guangdong, China				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 2325)				
TITLE	Ren,R.W., Fang,M.Y., Tian,X.D., Liu,J.W., Jiang,L.H., Lin,L.H. and Zhao,W.Z.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (16-JAN-2002) Department of Virology, The Military Medical Institute of Guangzhou Military District, Dong Guanzhuang Road 91, Guangzhou, Guangdong 5105407, China				
AUTHORS	Location/Qualifiers				
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ORIGIN					
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ACCESSION	AF509530				
VERSION	AF509530.1				
KEYWORDS	GI:21070436				
SOURCE	Dengue virus type 2				
ORGANISM	Dengue virus type 2				
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.				


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REFERENCE
AUTHORS Ren,R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Peng, C.
TITLE Isolation, identification and sequence analyses of dengue virus
JOURNAL type 2 strain GD19/2001
Unpublished
REFERENCE 1 (bases 1 to 2325)
AUTHORS Ren,R., Yu, F., Dong, T., Wei, L., Hua, J., Yan, H. and Peng, C.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Microbiology Department, The Military
Medical Institute of Guangzhou Military District, Dongguanhuang
Road, Guangzhou 510507, China
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ACCESSION AY044442
VERSION AY044442.1 GI:18643733
KEYWORDS
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Flavivirus; Dengue virus group.
1 (bases 1 to 2325)
Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.,
Holmes,E.C. and Gould,E.A.
Molecular epidemiology of dengue type 2 virus in Venezuela:
evidence for in situ virus evolution and recombination
J. Gen. Virol. 82 (Pt 12), 2945-2953 (2001)
21571640
MEDLINE 11714970
PUBMED
REFERENCE 2 (bases 1 to 2325)
AUTHORS Uzcatogui,N.Y., Camacho,D., Comach,G., Cuello de Uzcatogui,R.M.,
Holmes,E.C. and Gould,E.A.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2001) Flavivirus Group, CEH-Oxford, Mansfield
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Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67
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RESULT 11
AR232496 2357 bp RNA linear PAT 20-DEC-2002
LOCUS Sequence 1 from patent US 6455509.
DEFINITION AR232496
ACCESSION AR232496
VERSION AR232496.1 GI:27274633
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2357)
AUTHORS Kochel,T.J., Porter,K.R., Raviprakash,K., Hoffman,S.L. and
Hayes,C.G.
TITLE Dengue nucleic acid vaccines that induce neutralizing antibodies
JOURNAL Patent: US 6455509-A 1 24-SEP-2002;
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Db	 60 AATATGCTGAACCGCGAGAGAACCGCG 87	
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LOCUS	Dengue virus type 2 gene for polyprotein, partial cds, strain:New Guinea C.	
DEFINITION		
ACCESSION	D00346	
VERSION	D00346	
KEYWORDS		
SOURCE	D00346.1 GI:221230	
ORGANISM	Dengue virus type 2	
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	
AUTHORS	1 (bases 1 to 2357)	
TITLE	Gruenberg, A., Woo, W.S., Biedrzycka, A. and Wright, P.J.	
JOURNAL	Partial nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue virus type 2, New Guinea C and PUO-218 strains	
MEDLINE	J. Gen. Virol. 69 (Pt 6), 1391-1398 (1988)	
PUBMED	88258474	
COMMENT	3385407	
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Db	60 AATATGCTGAACCGCGAGAGAACCGCG 87	
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LOCUS	Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial cds	
DEFINITION		
ACCESSION	AY152036	
VERSION	AY152036.1	
KEYWORDS	GI:28170806	

RESULT 13		
DENJAMA	2469 bp	ss-RNA linear VRL 18-MAR-2002
LOCUS	Dengue virus type 2 ARAC 8110827 polyprotein gene, partial cds.	
DEFINITION		
ACCESSION	M15075	
VERSION	M15075.1	
KEYWORDS	GI:323650	
SOURCE	Dengue virus type 2	
ORGANISM	Dengue virus type 2	
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	
AUTHORS	1 (bases 1 to 2469)	
TITLE	Deubel, V., Kinney, R.M. and Trent, D.W.	
JOURNAL	Nucleotide sequence and deduced amino acid sequence of the structural proteins of dengue type 2 virus, Jamaica genotype	
MEDLINE	Virology 155 (2), 365-377 (1986)	
PUBMED	87071658	
FEATURES	Location/Qualifiers	
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Matches 28; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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Db	136 AATATGCTGAACCGCGAGAGAACCGCG 163	
RESULT 14		
AY152036S1	2552 bp	RNA linear VRL 29-SEP-2003
LOCUS	Dengue virus type 4 D4.20_1998 polyprotein precursor, gene, partial cds	
DEFINITION		
ACCESSION	AY152036	
VERSION	AY152036.1	
KEYWORDS	GI:28170806	


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TITLE      Direct Submission
JOURNAL    Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
           Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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           /note="acronym: DEN-4"
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           RAETWMSSEGAKHAQVESWILRNPGFALLAGFMAVMIQGTGRTVFFVLMVLVAP
           SYGMRVCVGNRDFVEGSGAWVDLVLEHGCVTTMAQKPTLDFLTTKTAKVAL
           LRTYCIBASINITTATRCPTQGEPLYLKEEQDQYICRRDVDRWGNGGCLFGKGV
           VTCAKFSCSGKITGNLVQIENLEYTVVTVVTHNGDTHAVGNDTSHGVTATITPRSPV
           EVKLPDYGELTLDCEPRSGIDFNEMILMKMKKTWL VHQWFLDPLPWTAGADTSEV
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           RMEKLRITKMSYTMCSGKFSIDKEMAEOTGHTTVVKVYKYGAGAPCKVPIEIRDVNE
           KVGVRVTSPLAENTSVNIELEPPFGDSYIVGVNSALTLHWFRKSSGKGMPE
           STYRGAKRMALGTANDFGVGLFTSLGKAVHQVFGSVYTTMFGVSWMIRILIGF
           LVLWIGTNSMTAMTCIAGVGITLFLGTQVADMGCVSVSWSGRELKCSGIFVVDN
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Query Match      100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 17
AY152048S1
LOCUS     Dengue virus type 4 D4.14_1998 polyprotein precursor, gene, partial
DEFINITION
ACCESSION AY152048.1 GI:28170833
VERSION   1
KEYWORDS  1 of 4
SEGMENT   Dengue virus type 4 (DEN-4)
SOURCE     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
           Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
           Selection-Driven Evolution of Emergent Dengue Virus
           Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
TITLE     Direct Submission
JOURNAL   Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
           Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES   Location/Qualifiers
source     1..2552
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           glycoprotein"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 18
AY152052S1
LOCUS     Dengue virus type 4 D4.12_1998 polyprotein precursor, gene, partial
DEFINITION
ACCESSION AY152052.1 GI:28170842
VERSION   1
KEYWORDS  1 of 4
SEGMENT   Dengue virus type 4 (DEN-4)
SOURCE     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
           Flavivirus; Dengue virus group.
REFERENCE 1 (bases 1 to 2552)
           Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
           Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
           Selection-Driven Evolution of Emergent Dengue Virus
           Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
TITLE     Direct Submission
JOURNAL   Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
           Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES   Location/Qualifiers
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RAETWMSSEGAKHAQRVESILRNPGFALLAGPMAYMIGOTGRTVFFVLMMLVAP
SYNRCVGVGNRDFVEGSGGAVDLVLEHGGCVTTMAQGRPTLDFELTKTTAKVAL
LRTYCIASISNITATRCPTQGEPLKEEQDQYICRRDVVDRGNGCGGLFGKGV
VTCAKFCSGKITGNLQIENLEYVTVVTHNGDTHAVGNDTSNHGVTATITPRSPV
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 19
AV152056S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.17_1998 polyprotein precursor, gene, partial cds.
ACCESSION AV152056
VERSION AV152056.1 GI:28170851
KEYWORDS
SEGMENT
SOURCE
ORGANISM
i of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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CDS

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SYNRCVGVGNRDFVEGSGGAVDLVLEHGGCVTTMAQGRPTLDFELTKTTAKVAL
LRTYCIASISNITATRCPTQGEPLKEEQDQYICRRDVVDRGNGCGGLFGKGV
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Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 20
AV152060S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.45_1998 polyprotein precursor, gene, partial cds.
ACCESSION AV152060
VERSION AV152060.1 GI:28170860
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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EVKLPDYGELTDCPEKSGIDFNEMILMKKKTWLHVKQWFLDPLPWTAGADTSEV
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 21
AY152064S1 2552 bp RNA linear VRL 29-SEP-2003
LOCUS
DEFINITION Dengue virus type 4 D4.47_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152064
VERSION AY152064.1 GI:28170869

KEYWORDS
SEGMENT
SOURCE

1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorrdam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629
REFERENCE
AUTHORS

2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorrdam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers
source

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/organism="Dengue virus type 4"
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KVGRVISTPLAENTNSVTNIELEPPFGDSYIVIGNSALTTLGHFRKSSIGRMFE
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 22
AY152068S1

LOCUS
DEFINITION Dengue virus type 4 D4.13_1998 polyprotein precursor, gene, partial cds.

ACCESSION AY152068
VERSION AY152068.1 GI:28170878

KEYWORDS
SEGMENT
SOURCE

1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorrdam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

12832629
REFERENCE
AUTHORS

2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorrdam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

Location/Qualifiers
source

1..>2552
/organism="Dengue virus type 4"
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RAETWMSSEGAHQAVESWILRNPGFALLAGPMAYMGQTQRTVFFVFLMVLAP
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EVKLPDYGELTDLCEPRSGIDFNEMILMKMKKTWLVKQWFLDPLPWTAGADTSEV
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 23	AY152072S1	2552 bp	RNA	linear	VRL 29-SEP-2003
LOCUS	AY152072S1				
DEFINITION	Dengue virus type 4 D4.46_1998 polyprotein precursor, gene, partial cds.				
ACCESSION	AY152072				
VERSION	AY152072.1	GI:28170887			
KEYWORDS					
SEGMENT	1 of 4				
SOURCE	Dengue virus type 4 (DEN-4)				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
AUTHORS	1. (bases 1 to 2552)				
TITLE	Direct Submission				
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
PUBMED	12832629				
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	/note="acronym: DEN-4"				
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ORIGIN					
Query Match	100.0%;	Score 28;	DB 14;	Length 2552;	
Best Local Similarity	100.0%;	Pred. No. 0.13;			
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	37	AATATGCTGAACCGGAGAGAAACCGCG	64		
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LOCUS	AY152076S1				
DEFINITION	Dengue virus type 4 D4.48_1998 polyprotein precursor, gene, partial cds.				
ACCESSION	AY152080				
VERSION	AY152080.1	GI:28170905			
KEYWORDS					
SEGMENT	1 of 4				
SOURCE	Dengue virus type 4 (DEN-4)				
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus type 4				
REFERENCE	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)				
AUTHORS	1. (bases 1 to 2552)				
TITLE	Direct Submission				
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico				
PUBMED	12832629				
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ORIGIN					
Query Match	100.0%;	Score 28;	DB 14;	Length 2552;	
Best Local Similarity	10				

REFERENCE	Flavivirus; Dengue virus group.	REFERENCE	2 (bases 1 to 2552)	2 (bases 1 to 2552)
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	
TITLE	Selection-Driven Evolution of Emergent Dengue Virus	TITLE	Direct Submission	
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)	JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico	
PUBMED	12832629	FEATURES	Location/Qualifiers	Location/Qualifiers
REFERENCE		source	1. .2552	1. .2552
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.		/organism="Dengue virus type 4"	/organism="Dengue virus type 4"
TITLE	Direct Submission		/mol_type="genomic RNA"	/mol_type="genomic RNA"
JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico		/isolate="D4.15_1998"	/isolate="D4.84_1994"
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ORIGIN		ORIGIN		
Query Match	100.0%; Score 28; DB 14; Length 2552;	Query Match	100.0%; Score 28; DB 14; Length 2552;	
Best Local Similarity	100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity	100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;	
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 AATATGCTGAAACGCGAGAGAAACCGCG 28	Qy	1 AATATGCTGAAACGCGAGAGAAACCGCG 28	
Db	37 AATATGCTGAAACGCGAGAGAAACCGCG 64	Db	37 AATATGCTGAAACGCGAGAGAAACCGCG 64	
RESULT 26		RESULT 27		
AY152084S1		AY152088S1		
LOCUS	Dengue virus type 4 D4.15_1998 polyprotein precursor, gene, partial cds.	LOCUS	Dengue virus type 4 D4.44_1998 polyprotein precursor, gene, partial cds.	
DEFINITION	Dengue virus type 4 D4.15_1998 polyprotein precursor, gene, partial cds.	DEFINITION	Dengue virus type 4 D4.44_1998 polyprotein precursor, gene, partial cds.	
ACCESSION	AY152084	ACCESSION	AY152088	
VERSION	AY152084.1	VERSION	AY152088.1	
KEYWORDS	1 of 4	KEYWORDS	1 of 4	
SEGMENT	Dengue virus type 4 (DEN-4)	SEGMENT	Dengue virus type 4 (DEN-4)	
SOURCE	Dengue virus type 4	SOURCE	Dengue virus type 4	
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.	
REFERENCE	1 (bases 1 to 2552)	REFERENCE	1 (bases 1 to 2552)	
AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	AUTHORS	Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.	
TITLE	Selection-Driven Evolution of Emergent Dengue Virus	TITLE	Direct Submission	
JOURNAL	Mol. Biol. Evol. 20 (10), 1650-1658 (2003)	JOURNAL	Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico	
PUBMED	12832629	FEATURES	Location/Qualifiers	Location/Qualifiers

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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64
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RESULT 30
AV152100S1
LOCUS
DEFINITION
Dengue virus type 4 D4.112_1995MQ polyprotein precursor, gene,
partial cds.
ACCESSION
AV152100
VERSION
AV152100.1 GI:28170950
SEGMENT
1 of 4
SOURCE
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
TITLE
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.13;
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Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64
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RESULT 31
AV152104S1

LOCUS
DEFINITION
Dengue virus type 4 D4.108_1996CR polyprotein precursor, gene,
partial cds.
ACCESSION
AV152104
VERSION
AV152104.1 GI:28170959
SEGMENT
1 of 4
SOURCE
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
TITLE
JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
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CDS

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 37 AATATGCTGAACGCGAGAGAAACCGCG 64

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AV152108S1
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DEFINITION
ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
PUBMED
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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DB 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 34
AV152116S1
LOCUS Dengue virus type 4 D4.36_1992 polyprotein precursor, gene, partial
DEFINITION
ACCESSION AY152112
VERSION AY152112.1 GI:28170977
KEYWORDS
SEGMENT
SOURCE
ORGANISM
1 of 4
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
PUBMED
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
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QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
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DB 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 34
AV152116S1
LOCUS Dengue virus type 4 D4.3_1987 polyprotein precursor, gene, partial
DEFINITION
ACCESSION AY152108
VERSION AY152108.1 GI:28170968
KEYWORDS
SEGMENT
SOURCE
ORGANISM
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Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
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Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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/db_xref="taxon:11070"
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AY152116S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.86_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152116
VERSION AY152116.1 GI:28170986
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 37 AATATGCTGAACGCGAGAGAACCGCG 64

RESULT 35
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DEFINITION Dengue virus type 4 D4.89_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152120
VERSION AY152120.1 GI:28170995
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
Db 37 AATATGCTGAACGCGAGAGAACCGCG 64

RESULT 36
LOCUS AY152124S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152124
VERSION AY152124.1 GI:28171004
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Selection-Driven Evolution of Emergent Dengue Virus Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
REFERENCE
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O. Direct Submission Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
Db 37 AATATGCTGAACGCGAGAGAACCGCG 64

SOURCE ORGANISM
Dengue virus type 4 (DEN-4)
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
REFERENCE
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REFERENCE
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Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
Db 37 AATATGCTGAACGCGAGAGAACCGCG 64

RESULT 36
LOCUS AY152124S1 2552 bp RNA linear VRL 29-SEP-2003
DEFINITION Dengue virus type 4 D4.80_1994 polyprotein precursor, gene, partial cds.
ACCESSION AY152124
VERSION AY152124.1 GI:28171004
KEYWORDS
SEGMENT
SOURCE
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Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
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REFERENCE
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACGCGAGAGAACCGCG 28
Db 37 AATATGCTGAACGCGAGAGAACCGCG 64

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
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TVTYKCPLLVNTPEPIDDCNCLTSTWYMGTCQSGRRERKRSVALTPHSGMGLT
RAETVMSSEGAWHQAQVESWILRNPFGFALLAGFAMYMIGQTGRTVFFVLMMLVAP
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EVKPDYGEFLTDCPEPSGIDFNMILMKKKTWLHKQWFLDLPFWTAGADTSEV
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1. .>2552
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCGAGAGAACCGCG 28
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Db 37 AATATGCTGAACCGCGAGAGAACCGCG 64

RESULT 37
AY152128S1
LOCUS
DEFINITION
Dengue virus type 4 D4.78_1994 polyprotein precursor, gene, partial
cds.
ACCESSION
AY152128
VERSION
AY152128.1 GI:28171013
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
ORGANISM
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
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JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
/isolate="D4.78.1994"
/db_xref="taxon:11070"
/country="Puerto Rico"
/note="acronym: DEN-4"
1. .>2552
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ORIGIN
Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGCGAGAGAACCGCG 28
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Db 37 AATATGCTGAACCGCGAGAGAACCGCG 64

RESULT 38
AY152132S1
LOCUS
DEFINITION
Dengue virus type 4 D4.77_1994 polyprotein precursor, gene, partial
cds.
ACCESSION
AY152132
VERSION
AY152132.1 GI:28171022
KEYWORDS
SEGMENT
SOURCE
1 of 4
Dengue virus type 4 (DEN-4)
ORGANISM
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.
1 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
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CDS

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 39
AY152136S1
LOCUS
DEFINITION
Dengue virus type 4 D4.76_1994 polyprotein precursor, gene, partial
cds.
AY152136
AY152136.1 GI:28171031
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
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VHTWTEQYKFPSPARLASAILNAHKDGVCGIRSTRLENVMWKQITNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
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Db 37 AATATGCTGAACCGGAGAGAAACCGCG 64
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RESULT 40
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LOCUS
DEFINITION
Dengue virus type 4 D4.82_1994 polyprotein precursor, gene, partial
cds.
AY152140
AY152140.1 GI:28171040
1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
AUTHORS
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M.,
Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico
FEATURES
Location/Qualifiers
1. .2552
/organism="Dengue virus type 4"
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 41
AY152144S1
LOCUS
DEFINITION
Dengue virus type 4 D4.83_1994 polyprotein precursor, gene, partial cds.
AY152144S1 2552 bp RNA linear VRL 29-SEP-2003

ACCESSION
AY152144

VERSION
AY152144.1 GI:28171049

KEYWORDS
1 of 4

SEGMENT
Dengue virus type 4 (DEN-4)

SOURCE
Dengue virus type 4

ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

TITLE
Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

PUBMED
12832629

REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

TITLE
Direct Submission

JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES
Location/Qualifiers

1..2552
/organism="Dengue virus type 4"
/mol_type="genomic RNA"
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100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RAETWMSSEGAKHAQVESWILRNPFGALLAGFMAYMIGOTGIQRTVFFVLMMLVAP
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ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KVGRVISTPLAENTSVTNIELEPPFGDSYIVIGVNSALTTLHFRKSGSSIGQMFE
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VHTWTEQYKQFOPESPARLASAILNAHKDRCVGIRSTRLENVMWVKQITNELN"

ORIGIN

Query Match 100.0%; Score 28; DB 14; Length 2552;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

Db 37 AATATGCTGAAACGCGAGAGAAACCGCG 64

RESULT 42
AY152148S1
LOCUS
DEFINITION
Dengue virus type 4 D4.81_1994 polyprotein precursor, gene, partial cds.
AY152148S1 2552 bp RNA linear VRL 29-SEP-2003

ACCESSION
AY152148

VERSION
AY152148.1 GI:28171058

KEYWORDS
1 of 4

SEGMENT
Dengue virus type 4 (DEN-4)

SOURCE
Dengue virus type 4

ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Dengue virus group.

REFERENCE
1 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

TITLE
Selection-Driven Evolution of Emergent Dengue Virus

JOURNAL
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)

PUBMED
12832629

REFERENCE
2 (bases 1 to 2552)
Bennett, S.N., Holmes, E.C., Chirivella, M., Rodriguez, D.M.,
Beltran, M., Vorndam, V., Gubler, D.J. and McMillan, W.O.

TITLE
Direct Submission

JOURNAL
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio
Piedras, PO Box 23360, San Juan 00931, Puerto Rico

FEATURES
Location/Qualifiers

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100.0%; Score 28; DB 14; Length 2552;
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CDS

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Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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 Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

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 AY152176.1 GI:28171121
 1 of 4
 DENGUE virus type 4 (DEN-4)
 DENGUE virus type 4
 Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
 1 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Selection-Driven Evolution of Emergent Dengue Virus
 Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
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 2 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Direct Submission
 Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
 Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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 Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

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 1 of 4
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 DENGUE virus type 4
 Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
 1 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Selection-Driven Evolution of Emergent Dengue Virus
 Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
 12832629
 2 (bases 1 to 2552)
 Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
 Direct Submission
 Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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ORIGIN
 Query Match 100.0%; Score 28; DB 14; Length 2552;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 37 AATATGCTGAACGCGAGAGAAACCGCG 64

RESULT 48
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 LOCUS
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 DENGUE virus type 4 D4.27_1992 polyprotein precursor, gene, partial cds.
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 DENGUE virus

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Query Match	100.0%;	Score 28;	DB 14;	Length 2552;
Best Local Similarity	100.0%;	Pred. No. 0.13;		
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AY152180
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1 of 4
Dengue virus type 4 (DEN-4)
Dengue virus type 4
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; Dengue virus group.
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Selection-Driven Evolution of Emergent Dengue Virus
Mol. Biol. Evol. 20 (10), 1650-1658 (2003)
12832629
2 (bases 1 to 2552)
Bennett,S.N., Holmes,E.C., Chirivella,M., Rodriguez,D.M., Beltran,M., Vorndam,V., Gubler,D.J. and McMillan,W.O.
Direct Submission
Submitted (18-SEP-2002) Biology, University of Puerto Rico - Rio Piedras, PO Box 23360, San Juan 00931, Puerto Rico
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)
724.058 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Post-processing: Minimum Match 0%

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Listing first 50 summaries

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- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	100.0	2357	8 ABX13740	Abx13740 Dengue vi
3	28	100.0	2423	12 ADG93319	Adg93319 DEN1 (Pue
4	28	100.0	3381	2 AAT47666	Aat47666 Dengue vi
5	28	100.0	3381	2 AAX25114	Aax25114 Dengue vi
6	28	100.0	3381	12 ADQ28715	Adq28715 Dengue vi
7	28	100.0	10616	10 AAD53912	Aad53912 Dengue vi
8	28	100.0	10648	4 AAD14612	Aad14612 Wild-type
9	28	100.0	10648	4 AAD14613	Aad14613 Attenuate
10	28	100.0	10649	10 AAD53911	Aad53911 Recombina
11	28	100.0	10649	10 AAD53910	Aad53910 Dengue vi
12	28	100.0	10717	4 AAD14605	Aad14605 Dengue vi
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21	28	100.0	10756	4 AAD14609	Aad14609 Dengue vi

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30	26	92.9	26	3 AAC68744	Aac68744 Dengue vi
31	26	92.9	28	2 AAT75917	Aat75917 DEN-2 clo
32	24.8	88.6	10699	4 AAD14610	Aad14610 Wild-type
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46	18.4	65.7	1443	9 ABX16417	Abx16417 DNA encod
47	18.4	65.7	1647	12 ADF44354	Adf44354 1647bp se
48	18.4	65.7	4512	2 AAQ22767	Aaq22767 JEV Nakay
49	18.4	65.7	10818	12 ADO07431	Ado07431 Japanese
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ALIGNMENTS

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ID ABX15698 standard; DNA; 28 BP.

XX AC ABX15698;

XX DT 31-MAR-2003 (first entry)

XX DE Dengue virus detection PCR primer #2.

XX PCR; primer; ss; reverse transcriptase; RT-PCR; dengue fever; DF;
KW dengue haemorrhagic fever; virus; viral detection.

XX OS Dengue virus.

XX PN US2002155435-A1.

XX PD 24-OCT-2002.

XX PF 28-FEB-2002; 2002US-00085944.

XX PR 01-MAR-2001; 2001US-0272535P.

XX PA (WANG/) WANG W.

XX PI Wang W;

XX WPI; 2003-182625/18.

XX New dengue virus-specific primers, useful for reverse transcriptase-
PT polymerase chain reaction assays, particularly for detecting or
PT quantitating dengue virus in a sample.

XX PS Claim 28; Page 1; 6pp; English.

XX This invention relates to novel Dengue virus reverse transcriptase (RT)
CC PCR primers which may be used to detect Dengue virus in a sample. Dengue
CC virus is a member of the flavivirus family and causes diseases including
CC dengue fever (DF) and dengue haemorrhagic fever. The invention also

CC comprises a method for detecting and quantitating dengue virus. The
 CC dengue virus-specific primers of the invention are useful in reverse
 CC transcriptase-polymerase chain reaction assays, particularly for
 CC detecting or quantitating dengue virus in a sample. The present sequence
 CC represents a dengue virus specific RT-PCR primer used in the method of
 CC the invention

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 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

RESULT 2
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 AC ABX13740;
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 DT 28-FEB-2003 (first entry)
 XX
 DE Dengue virus type 2 structural gene genome segment.
 XX
 KW Pharmaceutical; ds; immune response; immunogenic; envelope; membrane;
 KW PreM; dengue virus; Den; serotype; flavivirus; Flaviviridae; antigen;
 KW mosquito; Aedes aegyptii; acute undifferentiated fever;
 KW dengue haemorrhagic fever; DHF; dengue shock syndrome; DSS;
 KW immune enhancement phenomenon; DNA vaccine; gene therapy; vaccine;
 KW structural gene; virucide.

XX
 OS Dengue virus.
 XX
 PN US6455509-B1.
 XX
 PD 24-SEP-2002.
 XX
 PF 04-JUN-1997; 97US-00869423.
 XX
 PR 04-JUN-1996; 96US-0017839P.
 XX
 PA (USNA) US SEC OF NAVY.
 XX
 PI Kochel TJ, Porter KR, Raviprakash K, Hoffman SL, Hayes CG;
 XX
 DR WPI; 2003-066244/06.
 XX

PT New pharmaceutical compositions containing dengue nucleic acids, useful
 PT as a vaccine, particularly for inducing a protective immune response in
 PT mammalian subjects against the dengue virus infection.

XX
 PS Disclosure; Col 17-20; 26pp; English.
 XX
 CC The invention discloses a pharmaceutical composition capable of inducing
 CC an immune response in a mammalian subject, comprising an immunogenic
 CC amount of a eukaryotic plasmid expression vector in pharmaceutical form,
 CC which includes the envelope and membrane (preM) genes of a dengue type 1,
 CC 2, 3, or 4 virus. Dengue virus (Den) belongs to the flavivirus genus of
 CC the family Flaviviridae and is a positive strand RNA virus encoding ten
 CC proteins. These genes are translated as a polypeptide which is cleaved by
 CC host and viral proteases. The virus envelope protein is a major antigen
 CC which can be targeted by neutralising antibodies. The membrane protein
 CC also appears on the virion surface and is required for proper processing
 CC of the envelope protein. Dengue viruses are transmitted primarily by the
 CC mosquito, Aedes aegyptii, and can lead to human illnesses ranging from
 CC acute undifferentiated fever to dengue haemorrhagic fever (DHF) and
 CC dengue shock syndrome (DSS). Secondary infections, with a different
 CC serotype, may lead to an immune enhancement phenomenon. The compositions
 CC of the invention are DNA vaccines which are injected into the animal as a

CC technique of gene therapy. The composition is useful as a vaccine,
 CC particularly for inducing a protective immune response in mammalian
 CC subjects against the dengue virus infection. The sequence presented is
 CC the dengue virus type 2 (Den 2) structural gene genome segment
 XX

SQ Sequence 2357 BP; 782 A; 471 C; 595 G; 509 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 8; Length 2357;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 |||||
 Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 3
 ADG93319
 ID ADG93319 standard; DNA; 2423 BP.
 XX
 AC ADG93319;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE DEN1 (Puerto Rico/94) ME chimeric region DNA SeqID52.
 XX
 KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
 KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;
 KW dengue virus; delta30; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P2.

OS Dengue virus type 1.

XX
 PN WO2003092592-A2.
 XX
 PD 13-NOV-2003.
 XX
 PF 25-APR-2003; 2003WO-US013279.
 XX
 PR 03-MAY-2002; 2002US-0377860P.
 PR 23-DEC-2002; 2002US-0436500P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
 PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;
 PI Hanley K;

XX
 DR WPI; 2004-022612/02.
 DR P-PSDB; ADG93320.

XX
 PT New tetraivalent vaccine containing a common nucleotide deletion in the 3',
 PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
 PT of disease in humans caused by dengue virus, or for inducing immune
 PT response.

PS Disclosure; SEQ ID NO 52; 181pp; English.

XX
 CC This invention relates to a novel immunogenic composition being
 CC tetraivalent and containing a common nucleotide deletion in the 3',
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is
 CC unique since they contain a common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta30 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC) structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN1 ME chimeric region DNA which is related to
 CC the invention.

```

XX SQ Sequence 2423 BP; 747 A; 513 C; 636 G; 527 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 28; DB 12; Length 2423;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
Db 138 AATATGCTGAACCGGAGAGAAACCGCG 165

RESULT 4
AAT47666
ID AAT47666 standard; cDNA; 3381 BP.
XX AC AAT47666;
XX 17-OCT-2003 (revised)
DT 19-MAY-1997 (first entry)
XX Dengue virus serotype 2 PR159/S1 mutant sequence.
DE DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.
XX DEN-2; flavivirus; envelope protein; immunisation; vaccine; ss.
OS Dengue virus; serotype 2.
XX Key Location/Qualifiers
FH mutation 1216..1218
FT /*tag= a
FT /note= "codon GAG (Glu) at position 1216-1218 of PR159/S1
FT is GAA (Glu) in wild-type PR159"
FT mutation 1258..1260
FT /*tag= b
FT /note= "codon GTT (Val) at position 1258-1260 of PR159/S1
FT is GTG (Val) in wild-type PR159"
FT mutation 1762..1764
FT /*tag= c
FT /note= "codon GTT (Val) at position 1762-1764 of PR159/S1
FT is ATT (Ile) in wild-type PR159"
FT mutation 1927..1929
FT /*tag= d
FT /note= "codon AGC (Ser) at position 1927-1929 of PR159/S1
FT is AGT (Ser) in wild-type PR159"
XX WO9637221-A1.
XX 28-NOV-1996.
XX 24-MAY-1996; 96WO-US007627.
XX 24-MAY-1995; 95US-00448734.
PR 07-JUN-1995; 95US-00488807.
PR 10-JUL-1995; 95US-00500469.
XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX Ivy JM, Nakano E, Clements D;
XX WPI; 1997-020938/02.
DR P-FSDB; AAW09409.
XX Subunit vaccine against flavivirus infection - contg. recombinant
PT envelope protein in secretable form, used for immunising against
PT flavivirus infection.
XX Example 1; Fig 3A-D; 121pp; English.
XX A cDNA sequence of dengue virus serotype 2 (DEN-2) mutant strain PR159/S1
CC shows 4 differences from the wild-type DEN-2 PR159. This results in a
CC conservative mutation in domain B of S1 that may be involved in the
CC attenuation of this small-plaque, temp.-sensitive variant. The cDNA
CC encodes the capsid, pre-membrane, envelope and NS1 proteins (AAW09409) of

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CC the virus. The clone can be used to express recombinant secreted
CC polypeptides, comprising portions of the envelope protein (esp. domain B,
CC Gly298-Gly385), in eukaryotic hosts, e.g. yeast (see also AAT47667 and
CC AAT47703-04) and Drosophila, for use in subunit vaccines against viral
CC infection. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 28; DB 2; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACCGGAGAGAAACCGCG 28
Db 40 AATATGCTGAACCGGAGAGAAACCGCG 67

RESULT 5
AAX25114
ID AAX25114 standard; cDNA; 3381 BP.
XX AC AAX25114;
XX 17-OCT-2003 (revised)
DT 05-JUL-1999 (first entry)
XX Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.
DE Dengue virus serotype 2 PR159/S1 viral capsid, pprM, E, NS1 cDNA.
XX Flavivirus; envelope protein; vaccine; infection; diagnosis; ss.
XX Dengue virus; serotype 2.
XX WO9906068-A2.
XX 11-FEB-1999.
XX 27-JUL-1998; 98WO-US015447.
XX 31-JUL-1997; 97US-00904227.
XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
XX Ivy JM, Peters ID, Collier BG, McDonnell M, Harada KE;
XX WPI; 1999-153454/13.
DR P-FSDB; AAY05522.
XX Recombinant dimeric flaviviral envelope vaccine - comprising a dimeric
XX 80%E protein, useful for protecting against flavivirus, especially dengue
XX virus infections.
XX Example 1; Fig 3A-D; 60pp; English.
XX This cDNA sequence encodes the capsid, prM, envelope (E) and NS1 proteins
XX (see AAY05522) of serotype 2 dengue virus DEN-2 strain PR159/S1. This
XX strain served as the source for DEN-2 genes used in the invention. A
XX vaccine for protecting against flavivirus infection comprises a dimeric
XX 80% E protein that has been secreted as a recombinant protein from a
XX eukaryotic cell. 80% E indicates a C-terminally truncated flavivirus E.
XX The dimeric truncated E is formed; (1) by directly linking 2 tandem
XX copies of 80% E via a flexible tether; (2) via the formation of a leucine
XX zipper domain through the homodimeric association of 2 leucine zipper
XX helices each fused to the C-terminus of an 80% E molecule; or (3) via the
XX formation of a non-covalently associated four-helix bundle domain formed
XX upon association of two helix-turn-helix moieties attached to the C-
XX terminus of an 80% E molecule. Dimeric truncated DEN-2 E proteins are
XX efficiently secreted by recombinant cells, are easier to purify than
XX intracellular proteins, and generate a high titer neutralising antibody
XX response. The method is generally applicable to flaviviruses, in
XX particular dengue viruses such as DEN-2, where 80% E comprises amino
XX acids 1-395 of DEN-2 E. The products can also be used for diagnosis of
XX infection. (Updated on 17-OCT-2003 to standardise OS field)

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SQ Sequence 3381 BP; 1137 A; 702 C; 834 G; 708 T; 0 U; 0 Other;
 Query Match 100.0%; Score 28; DB 2; Length 3381;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AATATGCTGAAACGCGAGAAACCGCG 28
 |||||
 Db 40 AATATGCTGAAACGCGAGAAACCGCG 67

 RESULT 6
 ADQ28715
 ID ADQ28715 standard; DNA; 3381 BP.
 XX AC AC
 XX ADQ28715;
 XX
 DT 26-AUG-2004 (first entry)
 XX DE DE
 XX
 XX Dengue virus viral capsid, prM, E and NS1 genes.
 KW virucide; vaccine; Flavivirus; dimeric 80kE; Drosophila Schneider cell;
 KW immunogenic composition; multivalent immunodiagnostic; dengue virus;
 KW viral capsid; prM gene; E gene; NS1 gene; ds.
 XX
 XX Dengue virus.
 OS OS
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3381
 FT /*tag= a
 FT /product= "Dengue virus viral capsid, prM, E and NS1
 FT polyprotein"
 FT
 PN US6749857-B1.
 XX
 XX
 PD 15-JUN-2004.
 XX
 XX 18-AUG-1999; 99US-00376463.
 XX
 XX 31-JUL-1997; 97US-00904227.
 XX
 XX (HAWA-) HAWAII BIOTECHNOLOGY GROUP INC.
 XX
 XX Peters ID, Collier BG, Mcdonell M, Ivy JM, Harada K;
 XX
 XX WPI; 2004-438725/41.
 DR P-PSDB; ADQ28716.
 DR
 XX
 PT PT New vaccines for preventing or diagnosing infections caused by dengue
 PT virus comprises a therapeutic amount of a dimeric 80kE protein secreted
 PT from Drosophila Schneider cells.
 XX
 XX Example 1; SEQ ID NO 2; 47pp; English.
 XX
 CC The invention describes a vaccine that generates a protective,
 CC neutralising antibody response to a Flavivirus in a murine host. The
 CC vaccine comprises a therapeutic amount of a dimeric 80kE, the dimeric
 CC 80kE having been secreted as a recombinantly produced protein from
 CC Drosophila Schneider cells, and where 80kE represents the N-terminal 80k
 CC portion of the protein from residues 1-395. Also described are: an
 CC immunogenic polypeptide comprising the dimeric 80kE cited above; an
 CC immunogenic composition that generates a protective, neutralising
 CC antibody response to a Flavivirus in a murine host, comprising the above
 CC immunogenic polypeptide and a physiological carrier; a multivalent
 CC immunodiagnostic for the detection of Flavivirus, comprising at least 2
 CC of the above immunogenic polypeptides of at least 2 flaviviral serotypes;
 CC and an immunodiagnostic kit for the detection of Flavivirus in a test
 CC subject, comprising the above immunogenic or multivalent immunodiagnostic
 CC polypeptide, a suitable support phase coated with dimeric 80kE, and
 CC labeled antibodies immunoreactive to antibodies from the test subject.
 CC The composition is useful for preventing or diagnosing infections caused
 CC by dengue virus. This sequence encodes Dengue virus gene viral capsid,
 CC prM, E and NS1 genes for Dengue virus strain PR159/S1 used as the source

PD 28-NOV-2002.
XX
XX
PF 22-MAY-2002; 2002WO-US016308.
XX
XX
PR 22-MAY-2001; 2001US-0293049P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (BLAN/) BLANEY J E.
XX
XX Whitehead SS, Murphy BR, Hanley KA;
XX
XX WPI; 2003-120809/11.
DR P-PSDB; AAE35314.
XX
XX New mutated flavivirus, useful for fine tuning the attenuation and growth
PT characteristics of dengue virus vaccines for the prevention and/or
PT treatment of dengue virus infection.
XX
XX Disclosure; Page 135-138; 246pp; English.
XX
XX The present invention relates to novel mutated flaviviruses comprising a
CC phenotype in which the viral genome is modified by introduction of a
CC mutation, singly or in combination, taken from mutations from recombinant
CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
CC dengue type 4 virus. The methods and compositions of the invention are
CC useful for fine tuning the attenuation and growth characteristics of
CC dengue virus vaccines for the prevention and/or treatment of dengue virus
CC infection. The present sequence is Dengue virus type 4 strain
CC rDEN2/4delta30 DNA
XX
SQ Sequence 10616 BP; 3365 A; 2219 C; 2743 G; 2289 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 10616;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 8
AAD14612
ID AAD14612 standard; cDNA; 10648 BP.
XX
XX AAD14612;
XX
XX 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-4 1036 cDNA.
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal;
KW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type IV.
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /product= "DEN-4 1036 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07991.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 3; Page 373-389; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-4 (DEN-4) 1036 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10648 BP; 3294 A; 2213 C; 2810 G; 2331 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10648;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
DB 138 AATATGCTGAAACGCGAGAGAAACCGCG 165

RESULT 9
AAD14613
ID AAD14613 standard; cDNA; 10648 BP.
XX
XX AAD14613;
XX
XX 01-NOV-2001 (first entry)
DT
XX
XX Attenuated, vaccine-strain DEN-4 PDK-48 variant cDNA.
DE
XX
XX Flavivirus; Dengue virus-4; DEN-4; vaccine; infection; virucidal; mutein;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.
XX
XX Dengue virus; type IV.
OS
XX
XX Key Location/Qualifiers
FH 102..10265
FT /*tag= a
FT /product= "DEN-4 PDK-48 protein variant"
FT mutation replace(1211, T)
FT /*tag= b
FT mutation replace(1971, G)
FT /*tag= c
FT mutation replace(3182, G)
FT /*tag= d
FT mutation replace(6660, C)
FT /*tag= e
FT mutation replace(6957, A)
FT /*tag= f

CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain rDEN4 DNA
 XX

SQ Sequence 10649 BP; 3298 A; 2214 C; 2804 G; 2333 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 138 AATATGCTGAACGCGAGAGAAACCGCG 165

RESULT 11

AAAD53910
 ID AAD53910 standard; DNA; 10649 BP.

XX AC AAD53910;

XX DT 28-MAY-2003 (first entry)

XX DE Dengue virus type 4 strain 2A DNA.

XX KW Attenuation; growth; vaccine; infection; Dengue virus type 4; gene; ds.

XX OS Dengue virus.

FT FH Key Location/Qualifiers
 FT CDS 102..10649
 FT /*tag= a
 FT /product= "DEN4 strain 2A protein"
 FT mat_peptide 102..440
 FT /*tag= c
 FT /product= "Anchored capsid protein"
 FT mat_peptide 102..398
 FT /*tag= b
 FT /product= "Virion capsid protein"
 FT mat_peptide 441..938
 FT /*tag= d
 FT /product= "Membrane precursor protein"
 FT mat_peptide 714..938
 FT /*tag= e
 FT /product= "Membrane protein"
 FT mat_peptide 939..2423
 FT /*tag= f
 FT /product= "Envelope protein"
 FT mat_peptide 2424..3479
 FT /*tag= g
 FT /product= "NS1 protein"
 FT mat_peptide 3480..4133
 FT /*tag= h
 FT /product= "NS2A protein"
 FT mat_peptide 4134..4523
 FT /*tag= i
 FT /product= "NS2B protein"
 FT mat_peptide 4524..6377
 FT /*tag= j
 FT /product= "NS3 protein"
 FT mat_peptide 6378..6758
 FT /*tag= k
 FT /product= "NS4A protein"
 FT mat_peptide 6759..6827
 FT /*tag= l
 FT /product= "2K protein"
 FT mat_peptide 6828..7562
 FT /*tag= m
 FT /product= "NS4B protein"
 FT mat_peptide 7563..10262
 FT /*tag= n
 FT /product= "NS5 protein"

PN WO200295075-A1.
 XX PD 28-NOV-2002.
 XX PF 22-MAY-2002; 2002WO-US016308.
 XX PR 22-MAY-2001; 2001US-0293049P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (BLAN/) BLANEY J E.
 XX PI Whitehead SS, Murphy BR, Hanley KA;
 XX WPI; 2003-120809/11.
 DR P-FSDB; AAE35312.

XX New mutated flavivirus, useful for fine tuning the attenuation and growth
 PT characteristics of dengue virus vaccines for the prevention and/or
 PT treatment of dengue virus infection.

XX PS Disclosure; Page 123-126; 246pp; English.

XX The present invention relates to novel mutated flaviviruses comprising a
 CC phenotype in which the viral genome is modified by introduction of a
 CC mutation, singly or in combination, taken from mutations from recombinant
 CC virus bearing Vero adaptation mutations, putative Vero cell adaptation
 CC mutations of dengue type 4 virus (DEN4) or mutations known to attenuate
 CC dengue type 4 virus. The methods and compositions of the invention are
 CC useful for fine tuning the attenuation and growth characteristics of
 CC dengue virus vaccines for the prevention and/or treatment of dengue virus
 CC infection. The present sequence is Dengue virus type 4 strain 2A DNA

XX SQ Sequence 10649 BP; 3302 A; 2212 C; 2800 G; 2335 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 10; Length 10649;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 138 AATATGCTGAACGCGAGAGAGAAACCGCG 165

RESULT 12

AAAD14605

ID AAD14605 standard; cDNA; 10717 BP.

XX AC AAD14605;

XX DT 11-SEP-2003 (revised)

XX DT 01-NOV-2001 (first entry)

XX DE Dengue virus (DEN)-2/3-VP1 chimeric cDNA.

XX KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 XX immunogenic; viral disease; pharmaceutical; chimeric; ss.

XX OS Dengue virus; type II.

XX OS Dengue virus; type III.

XX OS Chimeric.

XX FH Key Location/Qualifiers

XX CDS 97..10266

XX /*tag= a

XX /product= "DEN-2/3-VP1 fusion protein"

XX PN WO200160847-A2.

XX PD 23-AUG-2001.

XX PF 16-FEB-2001; 2001WO-US005142.

XX PR 16-FEB-2000; 2000US-0182829P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX WPI; 2001-497162/54.
 XX P-PSDB; AAE07984.
 XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
 XX vaccinating against a range of dengue viruses.
 XX Example 2; Page 203-219; 470pp; English.
 XX The invention relates to avirulent, immunogenic flavivirus chimeras
 XX comprising amino acid mutations in the non-structural proteins of a
 XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
 XX structural genes of the virus are used as a backbone into which the
 XX structural protein genes of a second flavivirus strain are inserted.
 XX These chimeric viruses elicit pronounced immunogenicity but lack the
 XX accompanying clinical symptoms of viral disease. Attenuated chimeric
 XX flaviviruses are combined in a pharmaceutical composition to confer
 XX simultaneous immunity against several strains of pathogenic flaviviruses
 XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 XX flavivirus chimeras are also used as immunogens or multivalent vaccines
 XX to confer simultaneous protection against infections. The present cDNA
 XX sequence encodes dengue virus (DEN)-2/3-VPI fusion protein related to the
 XX invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
 XX comprising a valine at the non-structural protein (NS3)-250 and the
 XX premembrane/membrane protein (prM) and an envelope protein (E) from wild-
 XX type DEN-3 16562 virus. (Updated on 11-SEP-2003 to standardise OS field)
 XX Sequence 10717 BP; 3501 A; 2208 C; 2737 G; 2271 T; 0 U; 0 Other;
 XX Query Match 100.0%; Score 28; DB 4; Length 10717;
 XX Best Local Similarity 100.0%; Pred. No. 0.013;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
 RESULT 13
 AAQ12787
 ID AAQ12787 standard; RNA; 10723 BP.
 XX AC AAQ12787;
 XX 25-MAR-2003 (revised)
 XX 21-NOV-1991 (first entry)
 XX Dengue 2 virus genome.
 XX dengue virus; detection; consensus sequence; Flavivirus; PCR; ss.
 XX Dengue virus.
 OS
 XX Key Location/Qualifiers
 XX CDS 97..10272
 XX FT /tag= a
 XX FT 712..936
 XX mat_peptide /product= "M protein"
 XX FT 937..2421
 XX mat_peptide /tag= c
 XX FT /product= "E protein"
 XX FT 2422..3477
 XX mat_peptide /tag= d
 XX FT /product= "NS1"
 XX FT 3478..4131
 XX mat_peptide /tag= e
 XX FT /product= "NS2A"
 XX FT 4132..4518
 XX mat_peptide

FT /tag= f
 FT /product= "NS2B"
 FT 4519..6375
 FT mat_peptide /tag= g
 FT /product= "NS3"
 FT 6376..6825
 FT mat_peptide /tag= h
 FT /product= "NS4a"
 FT 6826..7569
 FT mat_peptide /tag= i
 FT /product= "NS4B"
 FT 7570..10269
 FT mat_peptide /tag= j
 FT /product= "NS5"
 XX FR2654113-A.
 XX 10-MAY-1991.
 XX 09-NOV-1989; 89FR-00914724.
 XX 09-NOV-1989; 89FR-00014724.
 XX (INSP) INST PASTEUR.
 XX Vincent D;
 PI WPI; 1991-225002/31.
 XX P-PSDB; AAR13166.
 DR DR
 XX Detection and identification of Flaviviridae in biological sample - by
 XX amplifying consensus sequence then hybridisation opt. followed by typing,
 XX e.g. sequencing amplified prod.
 XX Disclosure; Fig 3; 24pp; French.
 XX The dengue 2 virus is an example of a member of the Flaviviridae which
 XX can be identified using the probe pair of the invention. A species-
 XX specific sequence can be amplified using the claimed oligonucleotides as
 XX primers in a PCR reaction (see AAQ12788 and AAQ12789). Other viruses
 XX which can be identified include Japanese encephalitis virus and yellow
 XX fever virus. (Updated on 25-MAR-2003 to correct PR field.)
 XX Sequence 10723 BP; 3557 A; 2251 C; 2647 G; 3 T; 2249 U; 16 Other;
 SQ Query Match 100.0%; Score 28; DB 2; Length 10723;
 Best Local Similarity 89.3%; Pred. No. 0.013;
 Matches 25; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 Db 136 AAUAGUCGAAACGCGAGAGAAACCGCG 163
 RESULT 14
 AAT49303
 ID AAT49303 standard; cDNA; 10723 BP.
 XX AC AAT49303;
 XX 27-AUG-2003 (revised)
 XX 11-SEP-1997 (first entry)
 XX cDNA sequence encoding polyprotein of DEN-2 virus, strain 16681.
 XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 XX NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 XX chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 XX dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 XX DHF; DSS; ss.
 XX Dengue virus type 2 (strain 16681).
 OS

```

FH Key Location/Qualifiers
FT CDS
FT 97..10272
FT /*tag= a
FT /product= "DEN-2 polyprotein
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT FT FT
FT FT FT
XX FT FT
XX PN WO9640933-A1.
XX
XX PD 19-DEC-1996.
XX
XX PF 06-JUN-1996; 96WO-US009209.
XX
XX PR 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
DR P-PSDB; AAW06590.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 23; Page 107-121; 261pp; English.
XX
XX This sequence encodes the polyprotein from Dengue 2 virus, strain 16681.
CC The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3,
CC NS4A, NS4B and NS5 proteins. A clone of this wildtype viral sequence, PDK
CC -53, may be used in the production of a quadravalent vaccine which
CC provides immunity against all four serotypes of dengue virus. The vaccine
CC also comprises a chimeric DEN-2/1 virus, a chimeric DEN-2/3 virus, and/or
CC a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to
CC protect against infection by all four serotypes of dengue virus, DEN-1,
CC DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue
CC haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used
CC to produce the recombinant protein products of the DNA constructs which
CC are used in the vaccines. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2255 T; 0 U; 2 Other;

Query Match 100.0%; Score 28; DB 2; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAACCGCG 163

RESULT 15
AAT49304
ID AAT49304 standard; cDNA; 10723 BP.
XX
XX AC AAT49304;
XX
XX 27-AUG-2003 (revised)
DT 12-SEP-1997 (first entry)
XX
XX cDNA encoding polyprotein of attenuated DEN-2 virus, PDK-53.
XX
XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
KW DHF; DSS; ss.
XX
XX Dengue virus type 2 (strain 16681).
OS Synthetic.

```

```

XX Key Location/Qualifiers
FH mutation
FT /*tag= b
FT /note= "C>T mutation"
FT 97..10272
FT /*tag= a
FT /product= "DEN-2 attenuated polyprotein
FT /transl_except(pos:643..645, aa:Xaa)
FT /transl_except(pos:1135..1137, aa:Xaa)
FT /transl_except(pos:1393..1395, aa:Xaa)
FT /transl_except(pos:2809..2811, aa:Xaa)
FT /transl_except(pos:3040..3042, aa:Xaa)
FT /transl_except(pos:9208..9210, aa:Xaa)"
FT /note= "Xaa = unknown amino acid"
FT 524
FT mutation
FT /*tag= c
FT /note= "A>T mutation, causes Asp to Val substitution"
FT 2055
FT mutation
FT /*tag= d
FT /note= "C>T mutation"
FT 2579
FT mutation
FT /*tag= e
FT /note= "G>A mutation, causes Gly to Asp substitution"
FT 4018
FT mutation
FT /*tag= f
FT /note= "C>T mutation, causes Leu to Phe substitution"
FT 5547
FT mutation
FT /*tag= g
FT /note= "C>T mutation"
FT 6599
FT mutation
FT /*tag= h
FT /note= "G>C mutation, causes Gly to Ala substitution"
FT 8571
FT mutation
FT /*tag= i
FT /note= "C>T mutation"
XX
XX WO9640933-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US009209.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX 07-JUN-1995; 95US-00483292.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (UYMA-) UNIV MAHIDOL AT SALAYA.
XX
XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
PI Kinney R, Trent DW;
XX
XX WPI; 1997-052330/05.
DR P-PSDB; AAW06591.
XX
XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
PT quadravalent vaccine for protecting against Dengue virus infection.
XX
XX Claim 27; Page 122-136; 261pp; English.
XX
XX This sequence encodes the polyprotein from an attenuated derivative of
XX Dengue 2 virus, strain 16681. The derivative is designated PDK-53. The
XX polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A,
XX NS4B and NS5 proteins. The PDK-53 viral sequence may be used in the
XX production of a quadravalent vaccine which provides immunity against all
XX four serotypes of dengue virus. The vaccine also comprises a chimeric DEN
XX -2/1 virus, a chimeric DEN-2/3 virus, and/or a chimeric DEN-2/4 virus.
XX The new quadravalent vaccines are used to protect against infection by
XX all four serotypes of dengue virus, DEN-1, DEN-2, DEN-3 and DEN-4, which
XX can lead to dengue fever or fatal dengue haemorrhagic fever/dengue shock
XX syndrome (DHF/DSS). Host cells are used to produce the recombinant
XX protein products of the DNA constructs which are used in the vaccines.
XX (Updated on 27-AUG-2003 to correct OS field.)

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SQ Sequence 10723 BP; 3522 A; 2218 C; 2725 G; 2258 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAACGCCGAGAGAAACCGCG 28
|||||
DB 136 AATATGCTGAACGCCGAGAGAAACCGCG 163
|||||

RESULT 17
AAD14607
ID AAD14607 standard; cDNA; 10723 BP.
XX AAD14607;
XX AC
XX 11-SEP-2003 (revised)
DT DT
DT 01-NOV-2001 (first entry)
XX DE Wild-type, virulent DEN-2 16681 cDNA.
XX XX
XX Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal;
XW avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX OS
XX Dengue virus; type II.
XX Key Location/Qualifiers
PH 97..10272
FT CDS /*tag= a /product= "DEN-2 16681 protein"
FT FT
FT FT
XX WC0200160847-A2.
XX XX
XX PD 23-AUG-2001.
XX XX
XX PF 16-FEB-2001; 2001WO-US005142.
XX XX
XX PR 16-FEB-2000; 2000US-0182829P.
XX XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PA Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX PI WPI; 2001-497162/S4.
XX DR P-PSDB; AAE07986.
XX DR
XX PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX Example 3; Page 252-268; 470pp; English.
XX XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes wild-type, virulent dengue-2 (DEN-2) 16681 virus protein
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS3-NS4A-NS5) and finally a 3'
CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

```
SQ Sequence 10723 BP; 3553 A; 2200 C; 2713 G; 2257 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   |||||
DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 19
AAD14606
ID AAD14606 standard; cDNA; 10723 BP.
XX
AC AAD14606;
XX
DT 11-SEP-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Dengue virus (DEN)-2/4-VP1 chimeric cDNA.
XX
KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
OS Dengue virus; type II.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT 97..10272
FT /*tag= a
FT /product= "DEN-2/4-VP1 fusion protein"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07985.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 3; Page 227-243; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/4-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;

Query Match      100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
   |||||
DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 19
AAD14608
ID AAD14608 standard; cDNA; 10723 BP.
XX
AC AAD14608;
XX
DT 01-NOV-2001 (first entry)
DE Attenuated, vaccine-strain DEN-2 PDK-53 variant cDNA.
XX
KW Flavivirus; Dengue virus-2; DEN-2; vaccine; infection; virucidal; muten;
KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
KW ss.
XX
OS Dengue virus; type II.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(57, C)
FT /*tag= b
FT 97..10272
FT /*tag= a
FT /product= "DEN-2 PDK-53 protein variant"
XX
PN WO200160847-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005142.
XX
PR 16-FEB-2000; 2000US-0182829P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07987.
XX
PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
PS Example 1; Page 276-292; 470pp; English.
XX
CC The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/4-VP1 fusion protein related to the
CC invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone
CC comprising a valine at the non-structural protein (NS3)-250 and the
CC pre-membrane/membrane protein (prM) and an envelope protein (E) from wild-
CC type DEN-4 1036 virus. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10723 BP; 3493 A; 2186 C; 2752 G; 2292 T; 0 U; 0 Other;
```

CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes attenuated dengue-2 (DEN-2) PDK-53 protein variant
CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
CC contains 5' non-coding region followed by a capsid protein (C) encoding
CC region, premembrane/membrane protein (prM) encoding region, an envelope
CC protein (E) encoding region, followed by the region encoding non-
CC structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
CC non-coding region
XX
SQ Sequence 10723 BP; 3552 A; 2198 C; 2711 G; 2262 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 4; Length 10723;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
RESULT 20
ADN98025
ID ADN98025 standard; DNA; 10724 BP.
AC ADN98025;
XX
XX 29-JUN-2004 (first entry)
DT
XX
DE Dengue Virus isolate New Guinea complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
KW Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX Dengue virus.
OS
XX WO2004040263-A2.
XX
XX 13-MAY-2004.
XX
XX 31-OCT-2003; 2003WO-US034823.
XX
XX 31-OCT-2002; 2002US-0422755P.
PR 06-JUN-2003; 2003US-0476513P.
XX
XX (HEAL-) HEALTH RES INC.
PA
XX
XX Wong SJ, Pei-Yong S;
XX
XX WPI; 2004-400223/37.
XX
XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
PT reactive with antibody against WNV and cross-reactive with antibody
PT against a flavivirus, useful in diagnosing flavivirus infection caused by
PT DENV, WNV, JEV or SLEV.
XX
XX Disclosure; Fig 40; 212pp; English.
XX
CC The invention relates to a diagnostic kit comprising at least one
CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
CC envelope (E) protein or its immunogenic fragment having a native
CC conformation or non-denatured structure and that is reactive with
CC antibodies against WNV and cross-reactive with antibodies against a
CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to

CC the complete nucleotide sequence of the DENV isolate New Guinea.
XX
SQ Sequence 10724 BP; 3542 A; 2212 C; 2725 G; 2245 T; 0 U; 0 Other;
Query Match 100.0%; Score 28; DB 12; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 136 AATATGCTGAAACGCGAGAGAAACCGCG 163
RESULT 21
AAD14609
ID AAD14609 standard; cDNA; 10756 BP.
XX
AC AAD14609;
XX
XX 11-SEP-2003 (revised)
DT 06-AUG-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
XX Dengue virus (DEN)-2/WN-PP1 chimeric cDNA.
DE
XX
XX Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
XX
XX Dengue virus; type II.
OS
XX West Nile virus.
OS
XX Chimeric.
XX
XX Key Location/Qualifiers
FH CDS 97..10305
FT /*tag= a
FT /product= "DEN-2/WN-PP1 fusion protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
XX
XX WPI; 2001-497162/54.
DR P-PSDB; AAE07988.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
PT vaccinating against a range of dengue viruses.
XX
XX Example 6; Page 300-316; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
CC comprising amino acid mutations in the non-structural proteins of a
CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
CC structural genes of the virus are used as a backbone into which the
CC structural protein genes of a second flavivirus strain are inserted.
CC These chimeric viruses elicit pronounced immunogenicity but lack the
CC accompanying clinical symptoms of viral disease. Attenuated chimeric
CC flaviviruses are combined in a pharmaceutical composition to confer
CC simultaneous immunity against several strains of pathogenic flaviviruses
CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
CC flavivirus chimeras are also used as immunogens or multivalent vaccines
CC to confer simultaneous protection against infections. The present cDNA
CC sequence encodes dengue virus (DEN)-2/WN-PP1 fusion protein related to
CC the invention. This fusion protein contains DEN-2 16681 backbone and the
CC premembrane/membrane protein (prM) and an envelope protein (E) from West
CC Nile NY99. (Updated on 06-AUG-2003 to correct OS field.) (Updated on 11-

CC SEP-2003 to standardise OS field)

XX Query Match 100.0%; Score 28; DB 4; Length 10756;

SQ Sequence 10756 BP; 3422 A; 2254 C; 2788 G; 2292 T; 0 U; 0 Other;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 22

ADG93313

ID ADG93313 standard; DNA; 15159 BP.

XX AC ADG93313;

XX DT 11-MAR-2004 (first entry)

XX DE DEN2 (Tonga/74) cDNA plasmid P2.

XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;

XX KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;

XX KW dengue virus; delta30; attenuating mutation; humoral response;

XX KW cellular response; non-structural protein; structural protein;

XX KW dengue virus serotype; gene; ds; plasmid P2.

XX OS Dengue virus type 2.

XX PN WO2003092592-A2.

XX PD 13-NOV-2003.

XX PF 25-APR-2003; 2003WO-US013279.

XX PR 03-MAY-2002; 2002US-0377860P.

XX PR 23-DEC-2002; 2002US-0436500P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;

XX PI Hanley K;

XX DR WPI; 2004-022612/02.

XX DR P-PSDB; ADG93314.

XX PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'

XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing

XX PT of disease in humans caused by dengue virus, or for inducing immune

XX PT response.

XX PS Disclosure; SEQ ID NO 46; 181pp; English.

XX CC This invention relates to a novel immunogenic composition being

XX CC tetraivalent and containing a common nucleotide deletion in the 3'

XX CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be

XX CC useful for the development of compounds with a virucide or

XX CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is

XX CC useful in the prevention of disease in humans caused by dengue virus.

XX CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is

XX CC unique since they contain a common shared attenuating mutation which

XX CC eliminates the possibility of generating a virulent wild type virus in a

XX CC subject to be vaccinated since each component of the vaccine possesses

XX CC the same delta30 attenuating deletion mutation. The vaccine also is able

XX CC to induce humoral and cellular responses against all of the (non-

XX CC)structural proteins present in each dengue virus serotype. The present

XX CC sequence is that of the DEN2 cDNA plasmid P2 which is related to the

XX CC invention.

XX SQ Sequence 15159 BP; 4518 A; 3436 C; 3896 G; 3309 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 12; Length 15159;

Best Local Similarity 100.0%; Pred. No. 0.014; Indels 0; Gaps 0;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28

DB 136 AATATGCTGAAACGCGAGAGAAACCGCG 163

RESULT 23

ADG93317

ID ADG93317 standard; DNA; 2426 BP.

XX AC ADG93317;

XX DT 11-MAR-2004 (first entry)

XX DE DEN1 (Puerto Rico/94) CME chimeric region DNA SeqID50.

XX KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;

XX KW dengue type 4; virucide; immunostimulant; vaccine; tetraivalent vaccine;

XX KW dengue virus; delta30; attenuating mutation; humoral response;

XX KW cellular response; non-structural protein; structural protein;

XX KW dengue virus serotype; gene; ds; plasmid P2.

XX OS Dengue virus type 1.

XX PN WO2003092592-A2.

XX PD 13-NOV-2003.

XX PF 25-APR-2003; 2003WO-US013279.

XX PR 03-MAY-2002; 2002US-0377860P.

XX PR 23-DEC-2002; 2002US-0436500P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Blaney J;

XX PI Hanley K;

XX DR WPI; 2004-022612/02.

XX DR P-PSDB; ADG93318.

XX PT New tetraivalent vaccine containing a common nucleotide deletion in the 3'

XX PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing

XX PT of disease in humans caused by dengue virus, or for inducing immune

XX PT response.

XX PS Disclosure; SEQ ID NO 50; 181pp; English.

XX CC This invention relates to a novel immunogenic composition being

XX CC tetraivalent and containing a common nucleotide deletion in the 3'

XX CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be

XX CC useful for the development of compounds with a virucide or

XX CC immunostimulant activity or as a vaccine. The tetraivalent vaccine is

XX CC useful in the prevention of disease in humans caused by dengue virus.

XX CC Unlike previous tetraivalent vaccine, the new tetraivalent vaccine is

XX CC unique since they contain a common shared attenuating mutation which

XX CC eliminates the possibility of generating a virulent wild type virus in a

XX CC subject to be vaccinated since each component of the vaccine possesses

XX CC the same delta30 attenuating deletion mutation. The vaccine also is able

XX CC to induce humoral and cellular responses against all of the (non-

XX CC)structural proteins present in each dengue virus serotype. The present

XX CC sequence is that of the DEN1 CME chimeric region DNA which is related to

XX CC the invention.

XX SQ Sequence 2426 BP; 754 A; 509 C; 632 G; 531 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 12; Length 2426;

Best Local Similarity 96.4%; Pred. No. 0.059; Indels 1; Gaps 0;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 141 AATATGCTGAACGCGAGAGAAACCGCG 168

RESULT 24
 AAQ51476
 ID AAQ51476 standard; DNA; 10718 BP.
 XX
 AC AAQ51476;
 XX
 AC (revised)
 DT 27-AUG-2003
 DT 25-MAR-2003 (revised)
 DT 16-MAY-1994 (first entry)
 XX
 DE DEN1-S275/90 (ECACC V92042111).
 XX
 KW Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock syndrome;
 KW DSS; DEN1 polypeptides; ss.
 XX

Dengue virus type 2.
 OS
 OS
 FH Location/Qualifiers
 FT CDS 81..10271
 FT misc_RNA /*tag= a
 FT 81..422
 FT /*tag= b
 FT /label= C
 FT 123..422
 FT /*tag= C
 FT /label= C'
 FT 423..695
 FT /*tag= d
 FT /label= Prem
 FT 696..920
 FT /*tag= e
 FT /label= M
 FT 921..2402
 FT /*tag= f
 FT /label= E
 FT 2403..3464
 FT /*tag= g
 FT /label= NS1
 FT 3465..4112
 FT /*tag= h
 FT /label= NS2A
 FT 4113..4499
 FT /*tag= i
 FT /label= NS2B
 FT 4500..6359
 FT /*tag= j
 FT /label= NS3
 FT 6360..6809
 FT /*tag= k
 FT /label= NS4A
 FT 6810..7556
 FT /*tag= l
 FT /label= NS4B
 FT 7557..10268
 FT /*tag= m
 FT /label= NS5

XX WO9322440-A1.
 XX
 XX
 PD 11-NOV-1993.
 XX
 PF 28-APR-1993; 93WO-CA000182.
 XX
 PR 29-APR-1992; 92GB-00009243.
 XX
 PA (UYSI-) UNIV SINGAPORE NAT.
 XX
 PI Tan Y, Fu J, Tan B, Yap E, Chan Y;

XX WPI; 1993-368799/46.
 DR P-PSDB; AAR43662.
 XX
 PT New Dengue virus type 1 strain - used to obtain prods. for detection,
 PT diagnosis, vaccines and treatment involving virus.
 XX
 PS Claim 3; Page 20-34; 55pp; English.
 XX
 CC DEN1 virus, strain S275/90 was isolated from the serum of a dengue
 CC haemorrhagic fever (DHF) patient. RNA was isolated from the virus and
 CC used to prepare cDNA encoding DEN1 polypeptides. Dengue virus type 1
 CC prods. can be used for detection, diagnosis, vaccines (inactivated form)
 CC or treatment of DEN1 infections. The sequences given in AAQ51477-86 are
 CC oligonucleotides used to prepare cDNA fragments corresp. to Dengue virus
 CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 10718 BP; 3419 A; 2226 C; 2769 G; 2304 T; 0 U; 0 Other;
 Query Match 94.3%; Score 26.4; DB 2; Length 10718;
 Best Local Similarity 96.4%; Pred. No. 0.07;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 Db 120 AATATGCTGAACGCGAGAGAAACCGCG 147

RESULT 25
 AAD14603
 ID AAD14603 standard; cDNA; 10723 BP.
 XX
 AC AAD14603;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Dengue virus (DEN) -2/1-VP chimeric cDNA.
 XX
 KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX
 OS Dengue virus; type I.
 OS Dengue virus; type II.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2/1-VP fusion protein"
 XX
 PN WO200160847-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-US005142.
 XX
 PR 16-FEB-2000; 2000US-0182829P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX
 DR WPI; 2001-497162/54.
 DR P-PSDB; AAE07982.
 XX
 PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 PS Example 1; Page 155-170; 470pp; English.
 XX
 CC The invention relates to avirulent, immunogenic flavivirus chimeras

comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DENV)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from wild-type DEN-1 16007 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3514 A; 2229 C; 2722 G; 2258 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 26
 AAD14604
 ID AAD14604 standard; cDNA; 10723 BP.
 XX
 AC AAD14604;
 XX
 DT 11-SEP-2003 (revised)
 DT 01-NOV-2001 (first entry)
 XX
 DE Dengue virus (DENV)-2/1-VV chimeric cDNA.
 KW Flavivirus; Dengue virus; DEN; vaccine; infection; virucidal; avirulent;
 KW immunogenic; viral disease; pharmaceutical; chimeric; ss.
 XX
 OS Dengue virus; type I.
 OS Dengue virus; type II.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT CDS 97..10272
 FT /*tag= a
 FT /product= "DEN-2/1-VV fusion protein"
 XX
 PN WO200160847-A2.
 XX
 PD 23-AUG-2001.
 XX
 XX 16-FEB-2001; 2001WO-US005142.
 XX
 XX 16-FEB-2000; 2000US-0182829P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Kinney RM, Kinney CVH, Butrapet S, Gubler DL, Bhamarapravati N;
 XX
 DR WPI; 2001-497162/54.
 DR P-PSDB; AAE07983.
 XX
 PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 1; Page 179-195; 470pp; English.
 PS
 XX The invention relates to avirulent, immunogenic flavivirus chimeras

comprising amino acid mutations in the non-structural proteins of a flavivirus. Chimeric viruses containing the attenuation-mutated non-structural genes of the virus are used as a backbone into which the structural protein genes of a second flavivirus strain are inserted. These chimeric viruses elicit pronounced immunogenicity but lack the accompanying clinical symptoms of viral disease. Attenuated chimeric flaviviruses are combined in a pharmaceutical composition to confer simultaneous immunity against several strains of pathogenic flaviviruses such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic flavivirus chimeras are also used as immunogens or multivalent vaccines to confer simultaneous protection against infections. The present cDNA sequence encodes dengue virus (DENV)-2/1-VV fusion protein related to the invention. This fusion protein contains attenuated DEN-2 PDK-53V backbone comprising a valine at the non-structural protein (NS3)-250 and the capsid protein (C), premembrane/membrane protein (prM) and an envelope protein (E) from the vaccine strain of Dengue-1 (DEN-1) PDK-13 virus. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 10723 BP; 3514 A; 2228 C; 2722 G; 2259 T; 0 U; 0 Other;

Query Match 94.3%; Score 26.4; DB 4; Length 10723;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 Db 136 AATATGCTGAACGCGAGAGAAACCGCG 163

RESULT 27
 AAD14602
 ID AAD14602 standard; cDNA; 10735 BP.
 XX
 AC AAD14602;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Attenuated, vaccine-strain DEN-1 PDK-13 variant cDNA.
 KW Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal; mutein;
 KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;
 KW ss.
 XX
 OS Dengue virus; type I.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 95..10273
 FT /*tag= a
 FT /product= "DEN-1 PDK-13 protein variant"
 FT mutation replace(1323, T)
 FT /*tag= b
 FT mutation replace(1541, G)
 FT /*tag= c
 FT mutation replace(1543, A)
 FT /*tag= d
 FT mutation replace(1545, G)
 FT /*tag= e
 FT mutation replace(1567, A)
 FT /*tag= f
 FT mutation replace(1608, C)
 FT /*tag= g
 FT mutation replace(2363, A)
 FT /*tag= h
 FT mutation replace(2695, T)
 FT /*tag= i
 FT mutation replace(2782, C)
 FT /*tag= j
 FT mutation replace(5063, G)
 FT /*tag= k
 FT mutation replace(6048, A)
 FT /*tag= l
 FT mutation replace(6806, A)

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FT mutation /*tag= m
FT replace(7330, A)
FT /*tag= n
FT replace(9445, C)
FT /*tag= o
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07981.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 130-146; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes attenuated dengue-1 (DEN-1) PPK-13 virus protein variant
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region
XX
XX Query Match 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;
XX Sequence 10735 BP; 3429 A; 2231 C; 2776 G; 2299 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.071;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAACCGGAGAGAAACCGCG 161
XX
XX RESULT 28
XX RAD14601
XX ID AAD14601 standard; cDNA; 10735 BP.
XX
XX AC AAD14601;
XX
XX 11-SEP-2003 (revised)
XX DT 01-NOV-2001 (first entry)
XX
XX Wild-type, virulent DEN-1 16007 cDNA.
XX
XX Flavivirus; Dengue virus-1; DEN-1; vaccine; infection; virucidal;
XX avirulent; immunogenic; viral disease; pharmaceutical; ss.
XX
XX Dengue virus; type I.

```

```

XX Key Location/Qualifiers
XX CDS 95..10273
XX /*tag= a
XX /*product= "DEN-1 16007 protein"
XX
XX WO200160847-A2.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005142.
XX
XX 16-FEB-2000; 2000US-0182829P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;
XX
XX WPI; 2001-497162/54.
XX P-PSDB; AAE07980.
XX
XX Chimeric flaviviruses that are avirulent and immunogenic, useful for
XX vaccinating against a range of dengue viruses.
XX
XX Example 1; Page 106-122; 470pp; English.
XX
XX The invention relates to avirulent, immunogenic flavivirus chimeras
XX comprising amino acid mutations in the non-structural proteins of a
XX flavivirus. Chimeric viruses containing the attenuation-mutated non-
XX structural genes of the virus are used as a backbone into which the
XX structural protein genes of a second flavivirus strain are inserted.
XX These chimeric viruses elicit pronounced immunogenicity but lack the
XX accompanying clinical symptoms of viral disease. Attenuated chimeric
XX flaviviruses are combined in a pharmaceutical composition to confer
XX simultaneous immunity against several strains of pathogenic flaviviruses
XX such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
XX flavivirus chimeras are also used as immunogens or multivalent vaccines
XX to confer simultaneous protection against infections. The present cDNA
XX sequence encodes wild-type, virulent dengue-1 (DEN-1) 16007 virus protein
XX used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1
XX to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome
XX contains 5' non-coding region followed by a capsid protein (C) encoding
XX region, premembrane/membrane protein (prM) encoding region, an envelope
XX protein (E) encoding region, followed by the region encoding non-
XX structural proteins (NS1-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'
XX non-coding region. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Query Match 3432 A; 2232 C; 2774 G; 2297 T; 0 U; 0 Other;
XX Sequence 10735 BP; 3432 A; 2232 C; 2774 G; 2297 T; 0 U; 0 Other;
XX
XX Query Match 94.3%; Score 26.4; DB 4; Length 10735;
XX Best Local Similarity 96.4%; Pred. No. 0.071;
XX Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 AATATGCTGAACCGGAGAGAAACCGCG 28
XX |||||
XX 134 AATATGCTGAACCGGAGAGAAACCGCG 161
XX
XX RESULT 29
XX ADN98024
XX ID ADN98024 standard; DNA; 10735 BP.
XX
XX AC ADN98024;
XX
XX 29-JUL-2004 (first entry)
XX DT
XX
XX Dengue Virus isolate WestPac complete genome sequence.
XX
XX ds; West Nile Virus; envelope protein; glycoprotein E; flavivirus;
XX Japanese encephalitis virus; Dengue virus; St Louis encephalitis virus.
XX
XX Dengue virus.
XX

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PN WO2004040263-A2.
 XX 13-MAY-2004.
 XX 31-OCT-2003; 2003WO-US034823.
 XX 31-OCT-2002; 2002US-0422755P.
 XX 06-JUN-2003; 2003US-0476513P.
 XX (HEAL-) HEALTH RES INC.
 XX
 XX Wong SJ, Pei-Yong S;
 XX WPI; 2004-400223/37.
 XX GENBANK; U88535.
 XX
 XX New diagnostic kit comprising West Nile Virus (WNV) envelope protein
 PT reactive with antibody against WNV and cross-reactive with antibody
 PT against a flavivirus, useful in diagnosing flavivirus infection caused by
 PT DENV, WNV, JEV or SLEV.
 XX
 XX Disclosure; Fig 39; 212pp; English.
 XX
 XX The invention relates to a diagnostic kit comprising at least one
 CC isolated and purified polypeptide comprising a West Nile Virus (WNV)
 CC envelope (E) protein or its immunogenic fragment having a native
 CC conformation or non-denatured structure and that is reactive with
 CC antibodies against WNV and cross-reactive with antibodies against a
 CC flavivirus. The diagnostic kit is useful in diagnosing flavivirus
 CC infection caused by DENV, WNV, JEV or SLEV. This sequence corresponds to
 CC the complete nucleotide sequence of the DENV isolate WestPac.
 XX
 XX Sequence 10735 BP; 3421 A; 2245 C; 2774 G; 2295 T; 0 U; 0 Other;
 SQ

Query Match 94.3%; Score 26.4; DB 12; Length 10735;
 Best Local Similarity 96.4%; Pred. No. 0.071;
 Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 |||||
 DB 134 AATATGCTGAACGCGAGAGAAACCGCG 161
 |||||

RESULT 30
 AAC68744
 ID AAC68744 standard; DNA; 26 BP.
 AC AAC68744;
 XX
 XX 23-FEB-2001 (first entry)
 DT
 XX Dengue virus type 2 upper primer.
 DE
 XX Dengue virus; haemostatic; antibacterial; sepsis;
 KW immunosuppressive; immunomodulator; cardiac; cytostatic; cachexia;
 KW neuroprotective; respiratory; inflammation; infection; Crohn's disease;
 KW multiple sclerosis; autoimmune disorder; cardiovascular disorder;
 KW chronic myelogenous leukaemia; inflammatory bowel disease; PCR primer;
 KW ss.
 XX
 XX Dengue virus.
 OS
 XX WO200064479-A1.
 PN
 XX 02-NOV-2000.
 PD
 XX 26-APR-2000; 2000WO-US011700.
 XX
 XX 27-APR-1999; 99US-00301274.
 XX
 XX (ANTI-) ANTIBODY SYSTEMS INC.
 PA
 XX Fredeking TM, Ignatyev GM;
 PI

XX WPI; 2000-679646/66.
 XX
 XX Novel compositions comprising tetracycline or tetracycline-like compounds
 PT for the treatment and/or prevention of acute inflammatory responses and
 PT diseases, e.g. septic shock and immune complex-induced colitis.
 XX
 XX Example 2; Page 103; 183pp; English.
 PS
 XX
 XX The present sequence was used in an invention relating to novel
 CC compositions and methods containing tetracycline or tetracycline-like
 CC compounds for treating and/or preventing acute inflammatory responses and
 CC diseases. Such diseases include acute inflammatory conditions associated
 CC with viral haemorrhagic diseases (including diseases caused by
 CC Bunyaviridae, Filoviridae, Flaviviridae or Arenaviridae viruses);
 CC parasitic diseases, bacterial infections, sepsis, cachexia, autoimmune
 CC disorders, acute cardiovascular events, chronic myelogenous leukaemia and
 CC transplanted bone marrow-induced graft-versus-host disease, septic shock,
 CC immune complex-induced colitis, cerebrospinal fluid inflammation,
 CC multiple sclerosis, inflammatory responses associated with trauma,
 CC systemic inflammatory response syndrome (SIRS), adult respiratory
 CC distress syndrome (ARDS), acute liver failure, inflammatory bowel disease
 CC and Crohn's disease
 XX
 XX Sequence 26 BP; 11 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 SQ

Query Match 92.9%; Score 26; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
 |||||
 DB 1 AATATGCTGAACGCGAGAGAAACCG 26
 |||||

RESULT 31
 AAT75917
 ID AAT75917 standard; DNA; 28 BP.
 XX
 XX AAT75917;
 AC
 XX 15-SEP-1997 (first entry)
 DT
 XX DEN-2 cloning/sequencing sense primer, D2-134.
 DE
 XX
 XX Dengue 2 virus; polyprotein; capsid; prM; M; E; NS1; NS2A; NS2B; NS3;
 KW NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype;
 KW chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus;
 KW dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
 KW DHF; DSS; PCR; amplify; polymerase chain reaction; primer; ss.
 XX
 XX Synthetic.
 OS
 XX WO9640933-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX 06-JUN-1996; 96WO-US009209.
 XX
 XX 07-JUN-1995; 95US-00483292.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (UYMA-) UNIV MAHIDOL AT SALAYA.
 XX
 XX Bhamarapavati N, Butrapet S, Chang J, Gubler DJ, Halstead SB;
 PI Kinney R, Trent DW;
 XX
 XX WPI; 1997-052330/05.
 XX
 XX PDK-53, a clone of infectious attenuated Dengue 2 virus strain 16681 -
 PT also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a
 PT quadravalent vaccine for protecting against Dengue virus infection.
 XX

PS Example; Page 100; 261pp; English.

XX The sequences given in AAT75909-T76029 are primers which were used in the

CC amplification, cloning and sequencing of the Dengue-2 viral cDNA's of the

CC invention. The Dengue 2 viral DNA encodes a polyprotein which comprises

CC the capsid, prM, M, E, NS1, NS2A, NS2B, NS3, NS4A, NS4B and NS5 proteins.

CC The quadravalent vaccine of the invention comprises an attenuated Dengue

CC virus clone, PDK-53, and a chimeric DEN-2/1 virus, a chimeric DEN-2/3

CC virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are

CC used to protect against infection by all four serotypes of dengue virus,

CC DEN-1, DEN-2, DEN-3 and DEN-4, which can lead to dengue fever or fatal

CC dengue haemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are

CC used to produce the recombinant protein products of the DNA constructs

CC which are used in the vaccines

XX

SQ Sequence 28 BP; 11 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 92.9%; Score 26; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AATATGCTGAAACGCGAGAGAAACCG 26

Db 3 AATATGCTGAAACGCGAGAGAAACCG 28

|||||

RESULT 32

AAD14610

ID AAD14610 standard; cDNA; 10699 BP.

XX

AC AAD14610;

XX

DT 11-SEP-2003 (revised)

DT 01-NOV-2001 (first entry)

XX

XX

DE Wild-type, virulent DEN-3 16562 cDNA.

XX

XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal;

KW avirulent; immunogenic; viral disease; pharmaceutical; ss.

XX

OS Dengue virus; type III.

XX

XX

FH Key Location/Qualifiers

FT CDS 95..10267

FT /*tag= a

FT /product= "DEN-3 16562 protein"

XX

XX WO200160847-A2.

XX

PD 23-AUG-2001.

XX

XX

PF 16-FEB-2001; 2001WO-US005142.

XX

PR 16-FEB-2000; 2000US-0182829P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;

XX

DR WPI; 2001-497162/54.

DR P-PSDB; AAE07989.

XX

XX Chimeric flaviviruses that are avirulent and immunogenic, useful for

PT vaccinating against a range of dengue viruses.

XX

XX

PS Example 2; Page 325-341; 470pp; English.

XX

CC The invention relates to avirulent, immunogenic flavivirus chimeras

CC comprising amino acid mutations in the non-structural proteins of a

CC flavivirus. Chimeric viruses containing the attenuation-mutated non-

CC structural genes of the virus are used as a backbone into which the

CC structural protein genes of a second flavivirus strain are inserted.

CC These chimeric viruses elicit pronounced immunogenicity but lack the

CC

CC accompanying clinical symptoms of viral disease. Attenuated chimeric

CC flaviviruses are combined in a pharmaceutical composition to confer

CC simultaneous immunity against several strains of pathogenic flaviviruses

CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic

CC flavivirus chimeras are also used as immunogens or multivalent vaccines

CC to confer simultaneous protection against infections. The present cDNA

CC sequence encodes wild-type, virulent dengue-3 (DEN-3) 16562 virus protein

CC used for constructing flavivirus chimeras. Dengue virus types 1-4 (DEN-1

CC to DEN-4) are mosquito-borne flavivirus pathogens. The flavivirus genome

CC contains 5' non-coding region followed by a capsid protein (C) encoding

CC region, premembrane/membrane protein (prM) encoding region, an envelope

CC protein (E) encoding region, followed by the region encoding non-

CC structural proteins (NS1-NS2A-NS2A-NS3-NS4A-NS4B-NS5) and finally a 3'

CC non-coding region. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 10699 BP; 3437 A; 2224 C; 2779 G; 2259 T; 0 U; 0 Other;

Query Match 88.6%; Score 24.8; DB 4; Length 10699;

Best Local Similarity 92.9%; Pred. No. 0.37;

Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AATATGCTGAAACGCGAGAGAAACCG 28

Db 134 AATATGCTGAAACGCGAGAGAAACCGTG 161

|||||

RESULT 33

AAD14611

ID AAD14611 standard; cDNA; 10699 BP.

XX

AC AAD14611;

XX

DT 01-NOV-2001 (first entry)

XX

DE Attenuated, vaccine-strain DEN-3 PGMK-30/FRhL-3 variant cDNA.

XX

XX Flavivirus; Dengue virus-3; DEN-3; vaccine; infection; virucidal; mutein;

KW avirulent; immunogenic; viral disease; pharmaceutical; mutant; variant;

XX ss.

XX

OS Dengue virus; type III.

XX

XX Synthetic.

XX

FH Key Location/Qualifiers

FT CDS 95..10267

FT /*tag= a

FT /product= "DEN-3 PGMK-30/FRhL-3 protein variant"

FT mutation replace(550, C)

FT /*tag= b

FT mutation replace(1813, G)

FT /*tag= c

FT mutation replace(1838, A)

FT /*tag= d

FT mutation replace(1913, G)

FT /*tag= e

FT mutation replace(2140, C)

FT /*tag= f

FT mutation replace(3725, T)

FT /*tag= g

FT mutation replace(4781, C)

FT /*tag= h

XX

XX WO200160847-A2.

PN

XX

XX 23-AUG-2001.

XX

XX 16-FEB-2001; 2001WO-US005142.

PF

XX 16-FEB-2000; 2000US-0182829P.

PR

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA

XX Kinney RM, Kinney CYH, Butrapet S, Gubler DL, Bhamarapavati N;

PI

XX WPI; 2001-497162/54.
 DR P-PSDB; AAE07990.
 XX
 PT Chimeric flaviviruses that are avirulent and immunogenic, useful for
 PT vaccinating against a range of dengue viruses.
 XX
 XX Example 4; Page 349-365; 470pp; English.
 XX
 CC The invention relates to avirulent, immunogenic flavivirus chimeras
 CC comprising amino acid mutations in the non-structural proteins of a
 CC flavivirus. Chimeric viruses containing the attenuation-mutated non-
 CC structural genes of the virus are used as a backbone into which the
 CC structural protein genes of a second flavivirus strain are inserted.
 CC These chimeric viruses elicit pronounced immunogenicity but lack the
 CC accompanying clinical symptoms of viral disease. Attenuated chimeric
 CC flaviviruses are combined in a pharmaceutical composition to confer
 CC simultaneous immunity against several strains of pathogenic flaviviruses
 CC such as dengue virus serotypes DEN-1, DEN-2, DEN-3 and DEN-4. Immunogenic
 CC flavivirus chimeras are also used as immunogens or multivalent vaccines
 CC to confer simultaneous protection against infections. The present CDNA
 CC sequence encodes attenuated dengue-3 (DEN-3) FGMK-30/FRHL-3 (30 passages
 CC in primary green monkey kidney (FGMK) cells, followed by 3 passages in
 CC foetus rhesus lung cells) virus protein variant used for constructing
 CC flavivirus chimeras. Dengue virus types 1-4 (DEN-1 to DEN-4) are mosquito
 CC -borne flavivirus pathogens. The flavivirus genome contains 5' non-coding
 CC region followed by a capsid protein (C) encoding region,
 CC premembrane/membrane protein (prM) encoding region, an envelope protein
 CC (E) encoding region, followed by the region encoding non-structural
 CC proteins (NS1-NS2A-NS2B-NS3-NS4A-NS4B-NS5) and finally a 3' non-coding
 CC region
 XX
 SQ Sequence 10699 BP; 3439 A; 2221 C; 2778 G; 2261 T; 0 U; 0 Other;
 Query Match 88.6%; Score 24.8; DB 4; Length 10699;
 Best Local Similarity 92.9%; Pred. No. 0.37;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 DB 134 AATATGCTGAAACGCGTGAGAAACCGTG 161
 RESULT 34
 ADG93315
 ID ADG93315 standard; DNA; 15153 BP.
 XX
 AC ADG93315;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE DEN3 (Sleman/78) cDNA plasmid P3.
 XX
 KW immunogenic composition; dengue type 1; dengue type 2; dengue type 3;
 KW dengue type 4; virucide; immunostimulant; vaccine; tetravalent vaccine;
 KW dengue virus; delta30; attenuating mutation; humoral response;
 KW cellular response; non-structural protein; structural protein;
 KW dengue virus serotype; gene; ds; plasmid P3.
 XX
 OS Dengue virus type 3.
 XX
 FN WO2003092592-A2.
 XX
 PD 13-NOV-2003.
 XX
 PF 25-APR-2003; 2003WO-US013279.
 XX
 PR 03-MAY-2002; 2002US-0377860P.
 PR 23-DEC-2002; 2002US-0436500P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Whitehead SS, Murphy BR, Markoff L, Falgout B, Bianey J;
 XX
 PI Hanley K;
 XX
 DR WPI; 2004-022612/02.
 DR P-PSDB; ADG93316.
 XX
 PT New tetravalent vaccine containing a common nucleotide deletion in the 3'
 PT untranslated region of dengue types 1, 2, 3, and 4, useful for preventing
 PT of disease in humans caused by dengue virus, or for inducing immune
 PT response.
 XX
 XX Disclosure; SEQ ID NO 48; 181pp; English.
 XX
 CC This invention relates to a novel immunogenic composition being
 CC tetravalent and containing a common nucleotide deletion in the 3'
 CC untranslated region of dengue types 1, 2, 3, and 4. The invention may be
 CC useful for the development of compounds with a virucide or
 CC immunostimulant activity or as a vaccine. The tetravalent vaccine is
 CC useful in the prevention of disease in humans caused by dengue virus.
 CC Unlike previous tetravalent vaccine, the new tetravalent vaccine is
 CC unique since they contain a common shared attenuating mutation which
 CC eliminates the possibility of generating a virulent wild type virus in a
 CC subject to be vaccinated since each component of the vaccine possesses
 CC the same delta30 attenuating deletion mutation. The vaccine also is able
 CC to induce humoral and cellular responses against all of the (non-
 CC) structural proteins present in each dengue virus serotype. The present
 CC sequence is that of the DEN3 cDNA plasmid P3 which is related to the
 CC invention.
 XX
 SQ Sequence 15153 BP; 4434 A; 3440 C; 3943 G; 3336 T; 0 U; 0 Other;
 Query Match 88.6%; Score 24.8; DB 12; Length 15153;
 Best Local Similarity 92.9%; Pred. No. 0.39;
 Matches 26; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
 DB 134 AATATGCTGAAACGCGTGAGAAACCGTG 161
 RESULT 35
 AAF88836
 ID AAF88836 standard; DNA; 72 BP.
 XX
 AC AAF88836;
 XX
 DT 09-JAN-2003 (first entry)
 XX
 DE Green fluorescent protein PCR primer #1.
 XX
 KW Replicon; structural region; vaccine; subgenomic replicon; gene therapy;
 KW structural protein; C protein; PreM protein; E protein; immunisation;
 KW GFP; green fluorescent protein; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 FN WO200272803-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 21-FEB-2002; 2002WO-US006962.
 XX
 PR 09-MAR-2001; 2001US-0274684P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Pang X, Dayton AI, Zhang M;
 XX
 DR WPI; 2002-723344/78.
 XX
 PT New subgenomic replicon of dengue virus origin comprising a deletion for
 PT the sequence coding for C, PreM and/or E structural proteins, useful as
 PT vaccines for immunization against dengue virus infection.
 XX
 XX

PS Example 2; Page 38; 66pp; English.

XX This invention describes a novel subgenomic replicon of dengue virus

CC origin comprising a deletion for the sequence coding for C, PreM and E

CC (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE). Structural

CC proteins, and/or which is adapted to receive at least a nucleotide

CC sequence without disrupting its replication capabilities. The products of

CC the invention can be used for constructing (1) a vaccine or a therapeutic

CC comprising the subgenomic replicon and a carrier; (2) a dengue virus-like

CC particle comprising the subgenomic replicon, and structural proteins of

CC the homologous dengue virus, which encapsulates the subgenomic replicon;

CC and (3) methods of immunisation and treatment comprising administering to

CC the individual the subgenomic replicon or the dengue virus like particle

CC cited above. The subgenomic replicons are useful in gene therapy as

CC vaccines for immunisation against dengue virus infection. This sequence

CC represents a PCR primer used with AAF88837 to amplify the green

CC fluorescent protein (GFP) gene cloned into the dengue virus delta-pre-M/E

CC replicon, at the site previously occupied by the pre-M/E genes

XX

SQ Sequence 72 BP; 26 A; 12 C; 24 G; 10 T; 0 U; 0 Other;

Query Match 78.6%; Score 22; DB 6; Length 72;

Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACCGGAGAGAA 22

Db 28 AATATGCTGAACCGGAGAGAA 49

|||||

RESULT 36

AAC44997/c

ID AAC44997 standard; DNA; 1083 BP.

XX

AC AAC44997;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44912.

XX

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 26-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127452P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130499P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 30-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 04-MAY-1999; 99US-0132407P.

PR 05-MAY-1999; 99US-0132484P.

PR 06-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 06-MAY-1999; 99US-0132487P.

PR 07-MAY-1999; 99US-0132863P.

PR 11-MAY-1999; 99US-0134256P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.

PR 21-MAY-1999; 99US-0135353P.

PR 24-MAY-1999; 99US-0135629P.

PR 25-MAY-1999; 99US-0136021P.

PR 27-MAY-1999; 99US-0136392P.

PR 28-MAY-1999; 99US-0136782P.

PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.

PR 04-JUN-1999; 99US-0137502P.

PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.

PR 10-JUN-1999; 99US-0138540P.

PR 10-JUN-1999; 99US-0138847P.

PR 14-JUN-1999; 99US-0139119P.

PR 16-JUN-1999; 99US-0139452P.

PR 16-JUN-1999; 99US-0139453P.

PR 17-JUN-1999; 99US-0139492P.

PR 18-JUN-1999; 99US-0139454P.

PR 18-JUN-1999; 99US-0139455P.

PR 18-JUN-1999; 99US-0139456P.

PR 18-JUN-1999; 99US-0139457P.

PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.

PR 18-JUN-1999; 99US-0139460P.

PR 18-JUN-1999; 99US-0139461P.

PR 18-JUN-1999; 99US-0139462P.

PR 18-JUN-1999; 99US-0139463P.

PR 18-JUN-1999; 99US-0139750P.

PR 18-JUN-1999; 99US-0139763P.

PR 21-JUN-1999; 99US-0139817P.

PR 22-JUN-1999; 99US-0139899P.

PR 23-JUN-1999; 99US-0140353P.

PR 23-JUN-1999; 99US-0140354P.

PR 24-JUN-1999; 99US-0140895P.

PR 28-JUN-1999; 99US-0140823P.

PR 29-JUN-1999; 99US-0140991P.

PR 30-JUN-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-0141842P.

PR 01-JUL-1999; 99US-0142154P.

PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.

PR 08-JUL-1999; 99US-0142803P.

PR 09-JUL-1999; 99US-0142920P.

PR 12-JUL-1999; 99US-0142977P.

PR 13-JUL-1999; 99US-0143542P.

PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.

PR 16-JUL-1999; 99US-0144085P.

PR 16-JUL-1999; 99US-0144086P.

PR 19-JUL-1999; 99US-0144325P.

PR 19-JUL-1999; 99US-0144331P.

PR 19-JUL-1999; 99US-0144332P.

PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144335P.

PR 20-JUL-1999; 99US-0144352P.

PR 20-JUL-1999; 99US-0144632P.

PR 20-JUL-1999; 99US-0144884P.

PR 21-JUL-1999; 99US-0144814P.

PR 21-JUL-1999; 99US-0145086P.

PR 21-JUL-1999; 99US-0145088P.

PR 21-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145087P.

PR 22-JUL-1999; 99US-0145089P.

PR 22-JUL-1999; 99US-0145192P.


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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145278P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149317P.
PR 18-AUG-1999; 99US-0149422P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.

PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.6%; Score 19.2; DB 3; Length 1083;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACC 25
   ||||| ||||| ||||| |||||
Db 34 ATATGCGAAACGAGAGAGAAAC 11

RESULT 37
ADL98061
ID ADL98061 standard; DNA; 19 BP.
XX AC ADL98061;
XX DT 03-JUN-2004 (first entry)
XX DE SCRO gene specific PCR primer SEQ ID NO:6.
XX KW strand specific amplification; convertible oligonucleotide;
XX KW multi-conformational chimeric nucleotide; hemi-nested primer; detection;
XX KW quantification; identification; drug evaluation;
XX KW viral replication inhibition; PCR; primer; ss.
XX OS Synthetic.
XX PN WO2004022784-A2.
XX PD 18-MAR-2004.
XX PF 04-SEP-2003; 2003WO-SG000209.
XX PD 06-SEP-2002; 2002US-0408818P.
XX (UYJO ) JOHNS HOPKINS SINGAPORE PTE LTD.
XX PI Anwar A, August JT, Too H;
XX WPI; 2004-315577/29.
XX Strand specific amplification, useful in detecting and quantifying
XX nucleic acids, comprises designing a convertible oligonucleotide based on
XX the target nucleic acid strand.
XX Disclosure; SEQ ID NO 6; 79pp; English.
XX The present invention describes a strand specific amplification method
XX which comprises: (a) determining nucleic acid sequences of a target
XX nucleic acid strand; (b) designing a convertible oligonucleotide based,
XX at least in part, on the target nucleic acid strand; (c) conducting a
XX transcription reaction utilising the convertible oligonucleotide and the
XX target nucleic acid strand to provide at least one resultant complementary
XX strand; (d) conducting an amplification reaction to amplify the at least
XX one resultant complementary strand; and (e) analysing the amplification
XX reaction. Also described: (1) a convertible oligonucleotide comprising a
XX first self-annealing portion and a second portion complementary, at least
XX in part, to a target nucleic acid sequence; and (2) designing multi-
XX conformational chimeric nucleotides and hemi-nested primers. The method
XX is useful for strand specific amplification. The method is useful in
```

CC detecting and quantifying nucleic acids, detecting and identifying
CC pathogens and in evaluating drugs that inhibit viral replication. The
CC present sequence is used in the exemplification of the present invention.
XX Sequence 19 BP; 8 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
SQ
Query Match 67.9%; Score 19; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 TGAACCGGAGAGAAACCG 26
Db 1 TGAACCGGAGAGAAACCG 19
RESULT 38
ABQ34003
ID ABQ34003 standard; DNA; 765 BP.
AC ABQ34003;
XX
XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20594.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX Homo sapiens.
OS
XX WO200218632-A2.
PN
XX 07-MAR-2002.
PD
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX 01-SEP-2000; 2000DE-01043826.
PR
XX 05-SEP-2000; 2000DE-01044543.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX WPI; 2002-371829/40.
DR
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX SQ Sequence 765 BP; 336 A; 230 C; 80 G; 119 T; 0 U; 0 Other;
Query Match 67.9%; Score 19; DB 6; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
Db 441 ATACGCGAAACGCGAAGCAACGCG 467
RESULT 39
ABQ34002/c
ID ABQ34002 standard; DNA; 765 BP.
XX
AC ABQ34002;
XX
XX 12-JUL-2002 (first entry)
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 20593.
XX Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX Homo sapiens.
OS
XX WO200218632-A2.
PN
XX 07-MAR-2002.
PD
XX 01-SEP-2001; 2001WO-EP010074.
PF
XX 01-SEP-2000; 2000DE-01043826.
PR
XX 05-SEP-2000; 2000DE-01044543.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI
XX WPI; 2002-371829/40.
DR
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention
XX SQ Sequence 765 BP; 119 A; 80 C; 230 G; 336 T; 0 U; 0 Other;

Query Match 67.9%; Score 19; DB 6; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAACCGC 28
||| ||||| ||||| |||||
DB 325 ATACGCCGAAACGCGAACGAAACCGC 299

RESULT 40

ADD46068
ID ADD46068 standard; DNA; 28564 BP.
XX AC ADD46068;
XX XX
DT 29-JAN-2004 (first entry)
XX XX
DE Human gene AL138478, SEQ ID NO 11743.

XX KW Human; ds; gene; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX XX

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; AL138478.

XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human DNA (shown in Table 2 of the
XX CC specification) which encodes one of the polypeptides of the invention
XX CC which is differentially expressed during pain. Note: The sequence data

CC for this patent did not form part of the printed specification, but was
CC obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 28564 BP; 7828 A; 6116 C; 6366 G; 8254 T; 0 U; 0 Other;

Query Match 67.9%; Score 19; DB 10; Length 28564;
Best Local Similarity 81.5%; Pred. No. 1.7e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGC 27

||| ||||| ||||| |||||
DB 7881 AAGATGTTGAAAGATGAGAGAAACCGC 7907

RESULT 41

AAC46148/c

ID AAC46148 standard; DNA; 1008 BP.

XX AC AAC46148;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49081.

XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 05-MAR-1999; 99US-0123180P.

XX PR 09-MAR-1999; 99US-0123548P.

XX PR 23-MAR-1999; 99US-0125788P.

XX PR 25-MAR-1999; 99US-0126264P.

XX PR 29-MAR-1999; 99US-0126785P.

XX PR 01-APR-1999; 99US-0127462P.

XX PR 06-APR-1999; 99US-0128234P.

XX PR 16-APR-1999; 99US-0129845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130449P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0130891P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 30-APR-1999; 99US-0132407P.

XX PR 04-MAY-1999; 99US-0132484P.

XX PR 05-MAY-1999; 99US-0132485P.

XX PR 06-MAY-1999; 99US-0132486P.

XX PR 06-MAY-1999; 99US-0132487P.

XX PR 07-MAY-1999; 99US-0132863P.

XX PR 11-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134221P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

XX PR 19-MAY-1999; 99US-0134941P.

XX PR 20-MAY-1999; 99US-0135124P.

XX PR 21-MAY-1999; 99US-0135353P.

XX PR 24-MAY-1999; 99US-0135629P.

XX PR 25-MAY-1999; 99US-0136021P.

XX PR 27-MAY-1999; 99US-0136392P.

XX PR 28-MAY-1999; 99US-0136782P.

XX PR 01-JUN-1999; 99US-0137222P.

PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142330P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145244P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.

PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149910P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 28-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match

67.1%; Score 18.8; DB 3; Length 1008;

```
Best Local Similarity 90.9%; Pred. NO. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAA 23
DB 71 ATATGCAAGAACGAGAGAA 50

RESULT 42
ABL29849
ID ABL29849 standard; DNA; 3002 BP.
XX AC ABL29849;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41020.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
XX PN New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX PS Claim 1; SEQ ID NO 41020; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABLI16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 3002 BP; 843 A; 773 C; 822 G; 564 T; 0 U; 0 Other;

Query Match 66.4%; Score 18.6; DB 4; Length 3002;
Best Local Similarity 84.0%; Pred. NO. 2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAAACCG 26
DB 253 ATATGCTGAACGGCAGAGAAACGAG 277

RESULT 43
ABL29848
ID ABL29848 standard; DNA; 7264 BP.
XX AC ABL29848;
XX DT 26-MAR-2002 (first entry)

Best Local Similarity 90.9%; Pred. NO. 1.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAA 23
DB 71 ATATGCAAGAACGAGAGAA 50

RESULT 44
AAA82355
ID AAA82355 standard; DNA; 449 BP.
XX AC AAA82355;
XX DT 04-DEC-2000 (first entry)
XX DE N. meningitidis partial DNA sequence gnm_902 SEQ ID NO:902.
XX KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX KW Meningococcus B; MenB; ds.
XX OS Neisseria meningitidis.
XX PN WO200022430-A2.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-US023573.

Query Match 66.4%; Score 18.6; DB 4; Length 7264;
Best Local Similarity 84.0%; Pred. NO. 2.2e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGGCAGAGAAACCG 26
DB 1253 ATATGCTGAACGGCAGAGAAACGAG 1277

RESULT 44
AAA82355
ID AAA82355 standard; DNA; 449 BP.
XX AC AAA82355;
XX DT 04-DEC-2000 (first entry)
XX DE N. meningitidis partial DNA sequence gnm_902 SEQ ID NO:902.
XX KW Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
XX KW Meningococcus B; MenB; ds.
XX OS Neisseria meningitidis.
XX PN WO200022430-A2.
XX PD 20-APR-2000.
XX PF 08-OCT-1999; 99WO-US023573.
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PN US2002142407-A1.
 XX 03-OCT-2002.
 PD 09-JAN-2002; 2002US-00042991.
 PF 24-MAY-2000; 2000US-00578533.
 PR (FIRM) FIRMENICH SA.
 XX Whitehead IM, Siusarenko AJ, Waepi U, Gaekin DJH, Brash AR;
 PI Tifet N;
 XX WPI: 2003-197989/19.
 DR P-PSDB; ABG74402.
 XX
 PT Cleaving 13-hydroperoxide of linoleic acid into aldehyde and
 PT oxocarboxylic acid, and preparing n-hexanal from 13-hydroperoxy-octadeca-
 PT 9,11-dienoic acid, using recombinant fatty acid 13-hydroperoxide lyase.
 XX
 PS Disclosure; Page 21-22; 35pp; English.
 XX
 CC The invention describes a method of cleaving 13-hydroperoxide (I) of
 CC linoleic or alpha-linolenic acid into 6C-aldehyde (A) and 12C-
 CC oxocarboxylic acid (B). The method involves the use of recombinant
 CC protein produced by a vector containing nucleic acid encoding fatty acid
 CC 13-hydroperoxide lyase (HPOU). The method is useful for cleaving 13-
 CC hydroperoxide of linoleic or alpha-linolenic acid into a 6C-aldehyde and
 CC a 12C-oxocarboxylic acid, and for preparing n-hexanal, 3-(Z)-hexen-1-al,
 CC 2-(E)-hexen-1-al, 6C-aldehyde, 12C-oxocarboxylic acid, or their
 CC corresponding alcohols from 13-hydroperoxy-octadeca-9,11-dienoic acid or
 CC 13 hydroperoxy-octadeca-9,11,15-trienoic acid. This sequence
 CC encodes green pepper 13-hydroperoxide lyase (13-HPOL)
 XX
 SQ Sequence 1443 BP; 418 A; 288 C; 295 G; 442 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4; DB 9; Length 1443;
 Best Local Similarity 78.6%; Pred. No. 2.2e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 |||||
 DB 933 AATATGCTGAGATGCAAGAGAACTGAG 960
 |||||
 RESULT 47
 ADF44354
 ID ADF44354 standard; DNA; 1647 BP.
 XX ADF44354;
 AC ADF44354;
 XX 12-FEB-2004 (first entry)
 DT 1647bp sense HPL gene from green pepper.
 DE transformed; transgenic plant; hydroperoxide lyase; HPL;
 XX volatile biosynthesis HPL enzyme; insect; extermination; isothiocyanate;
 KW agrochemical; gene; green pepper; ds.
 KW Capsicum annum.
 XX JP2003339260-A.
 PN 02-DEC-2003.
 PD 27-MAY-2002; 2002JP-00153094.
 PF 27-MAY-2002; 2002JP-00153094.
 PR (KYOU) UNIV KYOTO.
 PA WPI; 2004-039487/04.
 DR
 XX

PT A transformed plant in which hydroperoxide lyase gene coding for volatile
 PT biosynthesis hydroperoxide lyase is transduced in sense or antisense
 PT direction, useful in insect-extermination.
 XX Claim 3; SEQ ID NO 1; 20pp; Japanese.
 PS The invention relates to a novel transformed plant in which a
 CC hydroperoxide lyase (HPL) gene coding for a volatile biosynthesis HPL
 CC enzyme is transduced in the sense/antisense direction, where activity of
 CC the HPL enzyme is improved or reduced compared to wild-type plant. The
 CC invention further relates an insect-extermination method using the
 CC transformed plant. In the transformed plant, the HPL gene is transduced
 CC in the sense direction and has a fully defined sequence of 1647 base
 CC pairs as given in the specification, and is derived from green pepper.
 CC The HPL gene transduced in the antisense direction has a fully defined
 CC sequence of 1711 base pairs as given in the specification, and is derived
 CC from Arabidopsis thaliana. The biosynthesis of an isothiocyanate compound
 CC is promoted in the transformed plant compared to the wild-type plant. The
 CC transformed plant is a Brassicaceae plant such as A. thaliana. The
 CC transformed plant efficiently exterminates an insect pest and also
 CC effectively inhibits growth of an insect pest. The novel transformed
 CC plant reduces the usage of an agrochemical. This polynucleotide sequence
 CC represents the 1647bp HPL gene from a green pepper of the invention.
 XX
 SQ Sequence 1647 BP; 517 A; 314 C; 320 G; 496 T; 0 U; 0 Other;
 Query Match 65.7%; Score 18.4; DB 12; Length 1647;
 Best Local Similarity 78.6%; Pred. No. 2.3e+02;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATATGCTGAACCGGAGAGAAACCGCG 28
 |||||
 DB 977 AATATGCTGAGATGCAAGAGAACTGAG 1004
 |||||
 RESULT 48
 AAQ22767
 ID AAQ22767 standard; DNA; 4512 BP.
 XX AAQ22767;
 AC AAQ22767;
 XX 12-AUG-1992 (first entry)
 DT JEV Nakayama strain prM, E, NS1, NS2A, NS2B and C coding regions.
 DE Japanese Encephalitis Virus; vaccinia virus donor; plasmid pDr20; ss.
 XX Japanese encephalitis virus.
 OS WO9203545-A.
 PN 05-MAR-1992.
 PD 05-AUG-1991; 91WO-US005816.
 PF 15-AUG-1990; 90US-00567960.
 PR 06-JUN-1991; 91US-00711429.
 PR 13-JUN-1991; 91US-00714687.
 PR 17-JUL-1991; 91US-00729800.
 PR 05-AUG-1991; 91WO-UO005816.
 XX (VIRO-) VIROGENETICS CORP.
 PA Paoletti E, Pinc, Pinc, Pincus SE;
 PI WPI; 1992-096889/12.
 DR Recombinant pox-virus e.g. vaccinia, fowl-pox and canary-pox virus -
 PT contg. DNA from flavi-virus e.g. Japanese encephalitis and yellow fever
 PT virus, used as vaccine.
 XX Example 9; Fig 17; 117pp; English.
 PS

CC cDNA was prepared from genomic virion RNA obtained from suspension
CC cultures of C6/36 cells infected with a passage 55 suckling mouse brain
CC stock of the Nagayama strain of JEV. EcoRI linkers were ligated to the
CC cDNA fragments for cloning into pBR322. Recombinant plasmids were
CC transformed into E.coli DH5 cells. Plasmid pC20 contained 81 non-coding
CC nucleotides and the coding regions for C and pM. Sequence AAQ22767 is
CC that of the C coding region of pC20, combined with an updated sequence of
CC the pM, E, NS1, NS2A and NS2B coding regions of the Nagayama strain. The
CC sequence begins at the C protein Met initiation codon. A subfragment of
CC pC20 was cloned into pUC18 to give pDr20. This plasmid was then used in
CC the construction of novel recombinants JEV24, JEV27, JEV33 and JEV34.
CC These were transfected into vP410 infected cells to generate vP825,
CC vP829, vP857 and vP864, respectively
XX
SQ Sequence 4512 BP; 1192 A; 1055 C; 1253 G; 1012 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 2; Length 4512;
Best Local Similarity 78.6%; Pred. No. 2.5e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 43 AATATGCTGAAACGCGGCTTACCCCGCG 70
|||||

RESULT 49
ADO07431
ID ADO07431 standard; DNA; 10818 BP.

XX AC ADO07431;

XX DT 15-JUL-2004 (first entry)

XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 9.

XX KW antiinflammatory; neuroprotective; gene therapy;

XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX KW Japanese encephalitis.

XX OS Japanese encephalitis virus.

XX OS WO2004033690-A1.

XX PN 22-APR-2004.

XX PD 09-OCT-2003; 2003WO-KR002081.

XX PF 09-OCT-2002; 2002KR-00061589.

XX PR (CIBC-) CID CO LTD.

XX PA (LEES/) LEE S H.

XX PI Lee SH, Lee Y, Yun S;

XX PI WPI; 2004-340933/31.

XX DR New Japanese encephalitis virus genomic RNA, useful in developing
XX PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX PT Example 2; Page 145-152; 265pp; English.

XX PS The present invention relates to a genomic RNA of the Korean Japanese

XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.

XX SQ Sequence 10818 BP; 2991 A; 2491 C; 3075 G; 2261 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 12; Length 10818;
Best Local Similarity 78.6%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 88 AATATGCTGAAACGCGGCTTACCCCGCG 115
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RESULT 50

ADO07437

ID ADO07437 standard; DNA; 10968 BP.

XX AC ADO07437;

XX DT 15-JUL-2004 (first entry)

XX DE Japanese Encephalitis virus JEV coding sequence SEQ ID NO: 15.

XX KW antiinflammatory; neuroprotective; gene therapy;

XX KW Japanese Encephalitis virus; JEV; ds; gene; vaccine;

XX KW Japanese encephalitis.

XX OS Japanese encephalitis virus.

XX OS WO2004033690-A1.

XX PN 22-APR-2004.

XX PD 09-OCT-2003; 2003WO-KR002081.

XX PF 09-OCT-2002; 2002KR-00061589.

XX PR (CIBC-) CID CO LTD.

XX PA (LEES/) LEE S H.

XX PI Lee SH, Lee Y, Yun S;

XX PI WPI; 2004-340933/31.

XX DR New Japanese encephalitis virus genomic RNA, useful in developing
XX PT vaccines for and in diagnosing and treating Japanese encephalitis.
XX PT Claim 3; Page 154-161; 265pp; English.

XX PS The present invention relates to a genomic RNA of the Korean Japanese
XX CC Encephalitis Virus (JEV) isolate, composed of a 5' and 3' nontranslated
XX CC region (NTR) and a single polypeptide coding region. The JEV genomic RNA,
XX CC JEV cDNA and reagents are useful in developing vaccines for and in
XX CC diagnosing and treating Japanese encephalitis. The present sequence is a
XX CC sequence of the invention.

XX SQ Sequence 10968 BP; 3032 A; 2518 C; 3117 G; 2301 T; 0 U; 0 Other;

Query Match 65.7%; Score 18.4; DB 12; Length 10968;
Best Local Similarity 78.6%; Pred. No. 2.8e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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Db 138 AATATGCTGAAACGCGGCTTACCCCGCG 165
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Search completed: January 19, 2005, 13:12:16
Job time : 206 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:56:22 ; Search time 51 Seconds
(without alignments)
390.237 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgctgaacgcgagagaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Issued Patents NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2357	4	US-08-869-423-1
2	28	100.0	3381	3	US-08-937-195-1
3	28	100.0	3381	3	US-08-937-195-2
4	28	100.0	3381	3	US-08-915-152-1
5	28	100.0	3381	3	US-08-915-152-2
6	28	100.0	3381	4	US-09-376-463-2
7	28	100.0	3381	5	PCT-US96-07627-1
8	28	100.0	3381	5	PCT-US96-07627-2
9	26.4	94.3	10718	3	US-08-325-426B-1
10	18.6	66.4	1145	4	US-09-270-767-9819
11	18.4	65.7	1443	3	US-09-078-173A-11
12	18.4	65.7	1443	4	US-10-042-991-11
13	18.4	65.7	4512	1	US-08-224-391-52
14	18.4	65.7	4512	1	US-08-484-304-52
15	18.4	65.7	12980	3	US-08-811-566-5
16	18.4	65.7	12980	3	US-08-811-566-5
17	17.6	62.9	3351	4	US-09-583-110-2433
18	17.4	62.1	763	4	US-09-270-767-8086
19	17.4	62.1	763	4	US-09-270-767-8086
20	17.4	62.1	983	3	US-08-875-233-11
21	17.4	62.1	1227	4	US-09-328-352-1888
22	17.4	62.1	2646	4	US-09-221-017B-558
23	17.4	62.1	5026	4	US-09-549-872B-3
24	17.4	62.1	6612	4	US-09-549-872B-5
25	17.4	62.1	11207	4	US-09-549-872B-2
26	17.2	61.4	3243	1	US-08-611-107-32
27	17.2	61.4	24358	4	US-09-392-812A-1

ALIGNMENTS

RESULT 1

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US-08-869-423-1
; Sequence 1, Application US/08869423
; Patent No. 6455509
; GENERAL INFORMATION:
; APPLICANT: Kochei, Tadeusz
; APPLICANT: Porter, Kevin R.
; APPLICANT: Raviprakash, Kanakatte
; APPLICANT: Hoffman, Stephen L.
; APPLICANT: Hayes, Curtis G.
; TITLE OF INVENTION: Dengue Nucleic Acid Vaccines that Induce
; TITLE OF INVENTION: Neutralizing Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Naval Medical Res. & Dev. Cmd.
; STREET: 8901 Wisconsin Ave., Bldg. 1, T-12
; CITY: Bethesda
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20889-5606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,423
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,839
; FILING DATE: 04-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kalish, Daniel
; REGISTRATION NUMBER: 33,599
; REFERENCE/DOCKET NUMBER: NC 77,654
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 295-5642
; TELEFAX: (301) 295-1022
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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c 28 17 60.7 435 4 US-09-252-991A-1169 Sequence 1169, Ap
c 29 17 60.7 1725 4 US-09-623-034-1 Sequence 1, Appli
c 30 17 60.7 2355 3 US-08-913-159-12 Sequence 12, Appl
c 31 17 60.7 2409 4 US-09-252-991A-1259 Sequence 1259, Ap
c 32 17 60.7 3378 4 US-09-328-352-4107 Sequence 4107, Ap
c 33 16.8 60.0 287 4 US-09-313-294A-1156 Sequence 1156, Ap
c 34 16.8 60.0 936 4 US-09-252-991A-11497 Sequence 11497, A
c 35 16.8 60.0 1746 4 US-09-489-039A-6977 Sequence 6977, Ap
c 36 16.6 59.3 297 4 US-09-313-294A-522 Sequence 522, Ap
c 37 16.6 59.3 702 4 US-08-956-171E-314 Sequence 314, App
c 38 16.6 59.3 702 4 US-08-781-986A-314 Sequence 295, App
c 39 16.6 59.3 792 4 US-09-134-000C-295 Sequence 361, App
c 40 16.6 59.3 851 4 US-08-961-527-361 Sequence 214, App
c 41 16.6 59.3 2558 3 US-08-936-165A-214 Sequence 34, Appl
c 42 16.6 59.3 10091 3 US-09-058-489-34 Sequence 8875, Ap
c 43 16.4 58.6 424 4 US-09-270-767-8875 Sequence 24157, A
c 44 16.4 58.6 424 4 US-09-270-767-3544 Sequence 3544, Ap
c 45 16.4 58.6 592 4 US-09-270-767-18826 Sequence 18826, A
c 46 16.4 58.6 592 4 US-09-270-767-18826 Sequence 105, App
c 47 16.4 58.6 652 4 US-09-221-017B-105 Sequence 1631, Ap
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c 49 16.4 58.6 977 4 US-09-270-767-16913 Sequence 710, App
c 50 16.4 58.6 1404 4 US-09-620-312D-710

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MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: New Guinea C
POSITION IN GENOME:
CHROMOSOME/SEGMENT: PreM and Envelope
MAP POSITION: 330-2446
UNITS: bp
PUBLICATION INFORMATION:
AUTHORS: Gruenberg, A
AUTHORS: Woo, W S
AUTHORS: Biedrzycka, A
AUTHORS: Wright, P J
TITLE: Partial nucleotide sequence and deduced amino
TITLE: acid sequence of the structural proteins of dengue
TITLE: virus type 2, New Guinea C and PUO-218 strains
JOURNAL: J. Gen. Virol.
VOLUME: 69
PAGES: 1391-1398
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Izrie, K
AUTHORS: Mohan, P M
AUTHORS: Sasaguri, Y
AUTHORS: Putnak, R
AUTHORS: Padmanabhan, R
TITLE: Sequence Analysis of Cloned dengue virus type

Patent No. 6455509
TITLE: 2 Genome (New Guinea-C strain)
JOURNAL: Gene
VOLUME: 75
ISSUE: 2
PAGES: 197-211
DATE: 1989
PUBLICATION INFORMATION:
AUTHORS: Yaegashi, T
AUTHORS: Vakharia, V N
AUTHORS: Page, K
AUTHORS: Sasaguri, Y
AUTHORS: Feighny, R
AUTHORS: Padmanabhan, R
JOURNAL: Gene
VOLUME: 46
ISSUE: 2-3
PAGES: 257-267
DATE: 1986

US-08-869-423-1
Query Match 100.0%; Score 28; DB 4; Length 2357;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 60 AATATGCTGAAACGCGAGAGAAACCGCG 87

RESULT 2
US-08-937-195-1
Sequence 1, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (Den-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PRI59/S1
FEATURE:

NAME/KEY: misc_feature
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OTHER INFORMATION: Wild-Type sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1260
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LOCATION: group(103, 1940, 1991, 2025)
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LOCATION: 841
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NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-937-195-1
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 40 AATATGCTGAACGGCAGAGAAACCGCG 67
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RESULT 3
US-08-937-195-2
Sequence 2, Application US/08937195
Patent No. 6136561
GENERAL INFORMATION:
APPLICANT: IVY, JOHN M.
APPLICANT: KAKANO, EILEEN
APPLICANT: CLEMENTS, DAVID
TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,195
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,807
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
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NAME/KEY: misc_feature
LOCATION: 1216..1218
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FEATURE:
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LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
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LOCATION: 343
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
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; PAGES: 167-180
; DATE: 1988
US-08-937-195-2

Query Match      100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 1, Application US/08915152
; Patent No. 6165477
; GENERAL INFORMATION:
; APPLICANT: IVY, JOHN M.
; APPLICANT: KAKANO, EILEEN
; TITLE OF INVENTION: SUBUNIT VACCINE AGAINST DENGUE INFECTION
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,152
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/500,469
; FILING DATE: 10-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4733-0003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Dengue virus
; STRAIN: Serotype 2 (Den-2)
; IMMEDIATE SOURCE:
; CLONE: Den-2 PR159/S1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: group(103, 1940, 1991, 2025)
; OTHER INFORMATION: /note= "Positions in the S1 strain
; OTHER INFORMATION: representing corrections to the wild type DEN-2 PR159 strain
; OTHER INFORMATION: reported by Hahn(Citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1218
; OTHER INFORMATION: /note= "G is replaced by A for
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CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
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OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 PENNSYLVANIA AVENUE, NW, STE. 5500
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,152
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/500,469
FILING DATE: 10-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0003.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3381 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Dengue virus
STRAIN: Serotype 2 (DEN-2)
IMMEDIATE SOURCE:
CLONE: Den-2 PR159/S1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3381
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1216..1218
OTHER INFORMATION: /note= "GAG(coding for Glu) is
OTHER INFORMATION: replaced by GAA(coding for Glu) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1258..1260
OTHER INFORMATION: /note= "GTG(coding for Val) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1762..1764
OTHER INFORMATION: /note= "ATT(coding for Ile) is
OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1927..1929
OTHER INFORMATION: /note= "AGT(Coding for Ser) is
OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
OTHER INFORMATION: strain(Citation #1)"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for Capsid"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 343
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for preMembrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 616
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Membrane"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 841
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence of Envelope"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2326
OTHER INFORMATION: /note= "Start of coding strand
OTHER INFORMATION: sequence for NS1"
PUBLICATION INFORMATION:
AUTHORS: Hahn, Y.S.
JOURNAL: Virology
VOLUME: 162
PAGES: 167-180
DATE: 1988
US-08-915-152-2
Query Match 100.0%; Score 28; DB 3; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67
RESULT 6
US-09-376-463-2
Sequence 2, Application US/09376463
Patent No. 6749857
GENERAL INFORMATION:
APPLICANT: Hawaii Biotechnology Group, Inc.
APPLICANT: Peters, Iain
APPLICANT: Collier, Beth-Ann
APPLICANT: McDonnell, Michael
APPLICANT: Ivy, John
APPLICANT: Harada, Kent
TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
TITLE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
FILE REFERENCE: 24733-20005.20
CURRENT APPLICATION NUMBER: US/09/376,463
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 08/904,227
PRIOR FILING DATE: 1997-07-31
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 3381
TYPE: DNA
ORGANISM: Dengue virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3381)
US-09-376-463-2
Query Match 100.0%; Score 28; DB 4; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
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; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1762..1764
; OTHER INFORMATION: /note= "ATT(coding for Ile) is
; OTHER INFORMATION: replaced by GTT(coding for Val) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1927..1929
; OTHER INFORMATION: /note= "AGT(Coding for Ser) is
; OTHER INFORMATION: replaced by AGC(coding for Ser) for the wild-type DEN-2 PR159
; OTHER INFORMATION: strain(citation #1)"
; OTHER INFORMATION: /citation= ({1})
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for Capsid"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 343
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for preMembrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 616
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Membrane"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 841
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence of Envelope"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2326
; OTHER INFORMATION: /note= "Start of coding strand
; OTHER INFORMATION: sequence for NS1"
; PUBLICATION INFORMATION:
; AUTHORS: Hahn, Y.S.
; JOURNAL: Virology
; VOLUME: 162
; PAGES: 167-180
; DATE: 1988
PCT-US96-07627-2

Query Match 100.0%; Score 28; DB 5; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 9
US-08-325-426B-1
; Sequence 1, Application US/08325426B
; Patent No. 6017535
; GENERAL INFORMATION:
; APPLICANT: FU, Jianlin
; APPLICANT: TAN, Boon-Haun
; APPLICANT: YAP, Eu-Hian
; APPLICANT: CHAN, Yow-Cheong
; APPLICANT: TAN, Yin-Hwee
; TITLE OF INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
; TITLE OF INVENTION: (SINGAPORE STRAIN)
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON and VANDERHYE PC
; STREET: 8th FLOOR, 1100 NORTH GLEBE ROAD
```

```
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,426B
; FILING DATE: 16-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10718 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA sequence corresponding to
; MOLECULE TYPE: the genomic RNA of DEN1-S275/90
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORGANISM: Dengue Fever Virus Type 1
; STRAIN: S275/90
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 81..10268
; US-08-325-426B-1

Query Match 94.3%; Score 26.4; DB 3; Length 10718;
Best Local Similarity 96.4%; Pred. No. 0.0085;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 120 AATATGCTGAAACGCGAGAGAAACCGCG 147

RESULT 10
US-09-270-767-9819/c
; Sequence 9819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9819
; LENGTH: 1145
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-9819

Query Match 66.4%; Score 18.6; DB 4; Length 1145;
Best Local Similarity 84.0%; Pred. No. 21;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCG 26
| | | | | | | | | | | | | | | | | |
Db 452 ATATGCTGAAACGCGAGAGAAACCG 428

RESULT 11
US-09-078-173A-11
; Sequence 11, Application US/09078173A
; Patent No. 6200794
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
```

```
; APPLICANT: Duncan Gaskins
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001
; CURRENT APPLICATION NUMBER: US/09/078,173A
; CURRENT FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-09-078-173A-11

Query Match      65.7%; Score 18.4; DB 3; Length 1443;
Best Local Similarity 78.6%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
   |||||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 12
US-10-042-991-11
; Sequence 11, Application US/10042991
; Patent No. 6780621
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; TITLE OF INVENTION: LYASE AND USES THEREOF
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match      65.7%; Score 18.4; DB 4; Length 1443;
Best Local Similarity 78.6%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
   |||||
Db 933 AAAATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 13
US-08-224-391-52
; Sequence 52, Application US/08224391
; Patent No. 5744140
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America

; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
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; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4512 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-224-391-52

Query Match      65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
   |||||
Db 43 AATATGCTGAACGCGGCTTACCCCGCG 70

RESULT 14
US-08-484-304-52
; Sequence 52, Application US/08484304
; Patent No. 5744141
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Pincus, Steven E.
; TITLE OF INVENTION: FLAVIVIRUS RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,304
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,391
; FILING DATE:
; APPLICATION NUMBER: US 07/729,800
; FILING DATE: 17-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2340
; TELECOMMUNICATION INFORMATION:
```


TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 4512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-304-52

Query Match 65.7%; Score 18.4; DB 1; Length 4512;
Best Local Similarity 78.6%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 43 AATATGCTGAACGCGGCTTACCCGCG 70

RESULT 15

US-08-811-566-5/c
Sequence 5, Application US/08811566
Patent No. 6127116

GENERAL INFORMATION:
APPLICANT: Rice, Charles et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,566
FILING DATE: 03-MAR-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1113-1-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-811-566-5

Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTGAACGCGGATACCCGCG 9687

RESULT 16

US-09-034-756-5/c
Sequence 5, Application US/09034756
Patent No. 6392028
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/034,756
FILING DATE: 04-May-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-034-756-5

Query Match 65.7%; Score 18.4; DB 3; Length 12980;
Best Local Similarity 78.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 9714 AATATGCTGAACGCGGATACCCGCG 9687

RESULT 17

US-09-583-110-2433
Sequence 2433, Application US/09583110
Patent No. 6699703
GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATH00-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 2433
LENGTH: 3351
TYPE: DNA

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; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2433

Query Match      62.9%; Score 17.6; DB 4; Length 3351;
Best Local Similarity 83.3%; Pred. No. 77;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAAC 24
    |||||
Db 830 AATATGCTGAAAGCTCTTGAGAAAC 853

RESULT 18
US-09-270-767-8086
; Sequence 8086, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8086
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8086

Query Match      62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACGC 27
    |||||
Db 534 AAAATGCGAAACGCGCAACAAACGC 560

RESULT 19
US-09-270-767-23368
; Sequence 23368, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23368
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23368

Query Match      62.1%; Score 17.4; DB 4; Length 763;
Best Local Similarity 77.8%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACGC 27
    |||||
Db 534 AAAATGCGAAACGCGCAACAAACGC 560

RESULT 20
US-08-875-233-11
; Sequence 11, Application US/08875233
; Patent No. 6127601
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; APPLICANT: McMaster, J. Russell

```

```

; APPLICANT: Tricoli, David M
; APPLICANT: Reynolds, John F
; APPLICANT: Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; TITLE OF INVENTION: Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: CUCUMBER MOSAIC VIRUS
; STRAIN: WHITE LEAF
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..657
; PUBLICATION INFORMATION:
; AUTHORS: Quemada, H
; AUTHORS: Kearney, C
; AUTHORS: Gonsalves, D
; AUTHORS: Slightom, J
; TITLE: Nucleotide Sequences of the Coat Protein
; TITLE: Genes and Flanking Regions of Cucumber Mosaic
; JOURNAL: J. Gen. Virol.
; VOLUME: 70
; PAGES: 1065-1073
; DATE: 1989
US-08-875-233-11

Query Match      62.1%; Score 17.4; DB 3; Length 983;
Best Local Similarity 77.8%; Pred. No. 74;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
    |||||
Db 113 AGATGCTGAAACTCAATAGAACCTCG 139

RESULT 21
US-09-328-352-1888/c
; Sequence 1888, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

```

FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1888
LENGTH: 1227
TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-1888

Query Match 62.1%; Score 17.4; DB 4; Length 1227;
Best Local Similarity 77.8%; Pred. No. 77;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACCGGAGAGAAACCGC 27
|||||
DB 964 AATATGCAAAACCGGAGAGAAACCGC 938
|||||

RESULT 22
US-09-221-017B-558
Sequence 558, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: Ross, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 558:
SEQUENCE CHARACTERISTICS:
LENGTH: 2646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1...2646
US-09-221-017B-558

Query Match 62.1%; Score 17.4; DB 4; Length 2646;
Best Local Similarity 77.8%; Pred. No. 90;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 AATATGCTGAAACCGGAGAGAAACCGC 28
|||||
DB 1472 ACAGATGAAAGCGGAGAAATCCGCG 1498
|||||

RESULT 23
US-09-549-872B-3
Sequence 3, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 5026
TYPE: DNA
ORGANISM: Caenorhabditis elegans
US-09-549-872B-3

Query Match 62.1%; Score 17.4; DB 4; Length 5026;
Best Local Similarity 94.7%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 AAACCGCGAGAGAAACCGCG 28
|||||
DB 2034 AAACCGCGAGAGAAACCGCG 2052
|||||

RESULT 24
US-09-549-872B-5
Sequence 5, Application US/09549872B
Patent No. 6540996
GENERAL INFORMATION:
APPLICANT: Zwaal, Richard
APPLICANT: Groenen, Jose
APPLICANT: Bogaert, Thierry
TITLE OF INVENTION: COMPOUND SCREENING METHODS
FILE REFERENCE: D00590/70008 (JRV/RE)
CURRENT APPLICATION NUMBER: US/09/549,872B
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: GB 9908670.4
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: US 60/129,596
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: GB 9912736.7
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 6612
TYPE: DNA

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; ORGANISM: Caenorhabditis elegans
US-09-549-872B-5

Query Match          62.1%; Score 17.4; DB 4; Length 6612;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 AAACGCGAGAGAAACCGCG 28
      |||||
Db      2646 AAACGCGAGAGAAACCGCG 2664

RESULT 25
US-09-549-872B-2
; Sequence 2, Application US/09549872B
; Patent No. 6540996
; GENERAL INFORMATION:
; APPLICANT: Zwaal, Richard
; APPLICANT: Groenert, Jose
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: COMPOUND SCREENING METHODS
; FILE REFERENCE: D00590/70008 (JRV/RE)
; CURRENT APPLICATION NUMBER: US/09/549,872B
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: GB 9908670.4
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 60/129,596
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: GB 9912736.7
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11207
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-549-872B-2

Query Match          62.1%; Score 17.4; DB 4; Length 11207;
Best Local Similarity 94.7%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      10 AAACGCGAGAGAAACCGCG 28
      |||||
Db      2640 AAACGCGAGAGAAACCGCG 2658

RESULT 26
US-08-611-107-32/c
; Sequence 32, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,107
; FILING DATE: Concurrently Herewith
```

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-611-107-32

Query Match          61.4%; Score 17.2; DB 1; Length 3243;
Best Local Similarity 86.4%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 TATGCTGAAAGCGGAGAGAAAC 24
      |||||
Db      926 TATGCTGAAAGCGGAGAGAAAC 905

RESULT 27
US-09-392-812A-1
; Sequence 1, Application US/09392812A
; Patent No. 6537778
; GENERAL INFORMATION:
; APPLICANT: Zuker, Richard G.
; APPLICANT: Walker, Richard G.
; APPLICANT: Willingham, Aaron
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A Eukaryotic Mechanosensory Transduction Channel
; FILE REFERENCE: 02307E-097600US
; CURRENT APPLICATION NUMBER: US/09/392,812A
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 24358
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: genomic nompC (no-mechanoreceptor potential C)
; OTHER INFORMATION: nucleotide sequence
US-09-392-812A-1

Query Match          61.4%; Score 17.2; DB 4; Length 24358;
Best Local Similarity 86.4%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 GCTGAAAGCGGAGAGAAACCGC 27
      |||||
Db      21468 GCAGAAAGCGGAGAGAAACCGC 21489

RESULT 28
US-09-252-991A-1169/c
; Sequence 1169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1169
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1169

Query Match 60.7%; Score 17; DB 4; Length 435;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 ATGCTGAACGCGAGAGAAACGCG 28
DB 425 AGGTCGAACGCGCGAGAAACGCG 401

RESULT 29
US-09-623-034-1
; Sequence 1, Application US/09623034
; Patent No. 6765128
; GENERAL INFORMATION:
; APPLICANT: Klessig, Daniel F.
; APPLICANT: Zhang, Shuqun
; TITLE OF INVENTION: METHODS OF USING A PATHOGEN-ACTIVATABLE
; TITLE OF INVENTION: MAP KINASE TO ENHANCE DISEASE RESISTANCE IN PLANTS
; FILE REFERENCE: RUT98-0073
; CURRENT APPLICATION NUMBER: US/09/623,034
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US99/03882
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 60/075,685
; PRIOR FILING DATE: 1998-02-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-623-034-1

Query Match 60.7%; Score 17; DB 4; Length 1725;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACC 25
DB 1231 AATATGCTTAACATAAGAGAAATC 1255

RESULT 30
US-08-913-159-12/c
; Sequence 12, Application US/08913159
; Patent No. 6300109
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Plasmid-derived type II
; TITLE OF INVENTION: restriction-modification systems from Lactococcus lactis
; NUMBER OF SEQUENCES: 14
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/913,159
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 0179/95
; FILING DATE: 17-FEB-1995
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2355 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Lactococcus lactis subsp. cremoris
; STRAIN: W39
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 744..1283
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /codon_start= 744
; OTHER INFORMATION: /product= "LlaDII restriction endonuclease"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ORF"
; OTHER INFORMATION: /number= 1
; OTHER INFORMATION: /standard_name= "Gene coding for R.LlaDII"
; OTHER INFORMATION: /label= r-llaDII
; OTHER INFORMATION: /note= "The first ten amino acids in this sequence may be
; OTHER INFORMATION: doubtful. However, from base 773 this reading frame gives a
; OTHER INFORMATION: homology with the Bsp6I endonuclease"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1392..2342
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /codon_start= 1392
; OTHER INFORMATION: /product= "LlaDII methylase"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; OTHER INFORMATION: /gene= "ORF"
; OTHER INFORMATION: /number= 2
; OTHER INFORMATION: /standard_name= "Gene coding for M.LlaDII"
; OTHER INFORMATION: /label= m-llaDII
; OTHER INFORMATION: /note= "The sequence shows 60 % identity and 76 % similarity
; OTHER INFORMATION: with the Bsp6I methylase."
US-08-913-159-12

Query Match 60.7%; Score 17; DB 3; Length 2355;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACC 25
DB 1326 AATATGATGAAAAGCGAGATAAAAC 1302

RESULT 31
US-09-252-991A-1259/c
; Sequence 1259, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1259
; LENGTH: 2409
```

```
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1259

Query Match      60.7%; Score 17; DB 4; Length 2409;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | | | | | |
Db 2208 AGGTGGAAGCGCGGAGAGAAACCGCG 2184

RESULT 32
US-09-328-352-4107
; Sequence 11497, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4107
; LENGTH: 3378
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4107

Query Match      60.7%; Score 17; DB 4; Length 3378;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 TATGCTGAACGCGAGAGAAACCGC 27
| | | | | | | | | | | | | | | | | |
Db 2791 TCTGCTGAACGGAAGAGAAAGC 2815

RESULT 33
US-09-313-294A-1156
; Sequence 1156, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1156
; LENGTH: 287
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700550474H1
US-09-313-294A-1156

Query Match      60.0%; Score 16.8; DB 4; Length 287;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 59 ATTATGCTGAACCTCGAGAGAACTGGG 86

RESULT 34
```

```
US-09-252-991A-11497/c
; Sequence 11497, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 11497
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11497

Query Match      60.0%; Score 16.8; DB 4; Length 936;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 901 AAGATGGAGAAACGAGCGGAAACCGCG 874

RESULT 35
US-09-489-039A-6977
; Sequence 6977, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6977
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6977

Query Match      60.0%; Score 16.8; DB 4; Length 1746;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
| | | | | | | | | | | | | | | | | |
Db 745 AATATGCTGCACGCGGAGAGCTGCGCG 772

RESULT 36
US-09-313-294A-522/c
; Sequence 522, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
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```
; SEQ ID NO 522
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549375H1
; LOCATION: 23, 27, 63, 79, 95, 102, 122, 160, 197, 247, 261
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-522

Query Match          59.3%; Score 16.6; DB 4; Length 297;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 GCTGAACCGAGAGAAACCGCG 28
Db 55 GCTGAACCGAGAGAGAAACCGCG 33

RESULT 37
US-08-956-171E-314
; Sequence 314, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 314:
US-08-956-171E-314

Query Match          59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;
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Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAA 23
Db 521 AAGATGTTGAAAAACGAGAGAAA 543

RESULT 38
US-08-781-986A-314
; Sequence 314, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 314:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-314

Query Match          59.3%; Score 16.6; DB 4; Length 702;
Best Local Similarity 82.6%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGAGAGAAA 23
Db 521 AAGATGTTGAAAAACGAGAGAAA 543

RESULT 39
US-09-134-000C-295
; Sequence 295, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
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; SEQ ID NO 295
; LENGTH: 792
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-295

Query Match      59.3%; Score 16.6; DB 4; Length 792;
Best Local Similarity 82.6%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||||| ||||| ||||| ||||| |||||
Db 641 AATATGCGAAATGCGACAAA 663

RESULT 40
US-08-961-527-361
; Sequence 361, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 361:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 851 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-361

Query Match      59.3%; Score 16.6; DB 4; Length 851;
Best Local Similarity 82.6%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ATATGCTGAAACGCGAGAGAAC 24
||||| ||||| ||||| ||||| |||||
Db 682 ACAAGCTAAACGCGACAGAAC 704

RESULT 41
US-08-936-165A-214/c
; Sequence 214, Application US/08936165A
; Patent No. 6348582
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Burnham, Martin
```

```
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Lonetto, Michael
; APPLICANT: Nicholas, Richard
; APPLICANT: Pratt, Julie
; APPLICANT: Reichard, Richard
; APPLICANT: Rosenberg, Martin
; APPLICANT: Ward, Judith
; TITLE OF INVENTION: Polypeptides and Their Uses
; TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
; NUMBER OF SEQUENCES: 534
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,165A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/027,032
; FILING DATE: 24-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2558 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-936-165A-214

Query Match      59.3%; Score 16.6; DB 3; Length 2558;
Best Local Similarity 82.6%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAA 23
||||| ||||| ||||| ||||| |||||
Db 2194 AAGATGTTGAAAAACGAGAGAAA 2172

RESULT 42
US-09-058-489-34
; Sequence 34, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; FILE REFERENCE: WHI97-08pA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 34
; LENGTH: 10091
; TYPE: DNA
; ORGANISM: Human
US-09-058-489-34

Query Match      59.3%; Score 16.6; DB 3; Length 10091;
Best Local Similarity 82.6%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAA 23
Db 2890 AATATGCTAGAAAAGCTAGAGAAA 2912

RESULT 43
US-09-270-767-8875/c
; Sequence 8875, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8875
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8875

Query Match      58.6%; Score 16.4; DB 4; Length 424;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 27
Db 273 ATATGCTGAATGCAGGAGAGACG 248

RESULT 44
US-09-270-767-24157/c
; Sequence 24157, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24157
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-24157

Query Match      58.6%; Score 16.4; DB 4; Length 424;
Best Local Similarity 76.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAAACCG 27
Db 273 ATATGCTGAATGCAGGAGAGACG 248

RESULT 45
US-09-270-767-3544/c
; Sequence 3544, Application US/09270767
; Patent No. 6703491
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; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3544
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-3544

Query Match      58.6%; Score 16.4; DB 4; Length 592;
Best Local Similarity 76.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
Db 436 ATTATGTTGAAACGAGGGGAAAACG 411

RESULT 46
US-09-270-767-18826/c
; Sequence 18826, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18826
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-18826

Query Match      58.6%; Score 16.4; DB 4; Length 592;
Best Local Similarity 76.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCG 26
Db 436 ATTATGTTGAAACGAGGGGAAAACG 411

RESULT 47
US-09-221-017B-105/c
; Sequence 105, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221.017B
; FILING DATE: 23-DEC-1998
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORYPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...652
US-09-221-017B-105

Query Match 58.6%; Score 16.4; DB 4; Length 652;
Best Local Similarity 76.9%; Pred. No. 2.e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGAGGAAACCGC 27
|||||
Db 480 ATATAGTCAACCTGAGGAAACAGC 455

RESULT 48
US-09-270-767-1631/c
; Sequence 1631, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1631

Query Match 58.6%; Score 16.4; DB 4; Length 977;
Best Local Similarity 76.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGAGGAAACCGC 27
|||||
Db 387 ATTTCAGCAACTCGTGTGAACCGC 362

RESULT 49
US-09-270-767-16913/c
; Sequence 16913, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16913
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-16913

Query Match 58.6%; Score 16.4; DB 4; Length 977;
Best Local Similarity 76.9%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGAGGAAACCGC 27
|||||
Db 387 ATTTCAGCAACTCGTGTGAACCGC 362

RESULT 50
US-09-620-312D-710/c
; Sequence 710, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: Pt_FL_genes Version 1.0
; SEQ ID NO 710
; LENGTH: 1404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (104)..(916)
US-09-620-312D-710

Query Match 58.6%; Score 16.4; DB 4; Length 1404;
Best Local Similarity 76.9%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGGAGAGAAACCG 26
| | | | | | | | | | | | | | | | | | | | | |
Db 1245 AATAGGCTAAATGAAAAAGAAACCG 1220

Search completed: January 19, 2005, 13:55:03
Job time : 52 secs

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OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 13:08:52 ; Search time 207 Seconds
(without alignments)
777.222 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgctgaacgcgagagaacgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	13	US-10-085-944-2
2	28	100.0	3381	15	US-10-247-960-2
3	28	100.0	10724	18	US-10-699-550-4
4	26.4	94.3	10735	18	US-10-699-550-3
5	26	92.9	26	9	US-09-840-707A-23
6	26	92.9	26	14	US-10-038-557A-23
7	22	78.6	72	18	US-10-656-721-26
8	19.6	70.0	594	18	US-10-425-115-108018
c 9	19	67.9	765	18	US-10-363-345A-20593
c 10	19	67.9	765	18	US-10-363-345A-20594
c 11	18.8	67.1	1428	15	US-10-369-493-32952
12	18.6	66.4	1602	15	US-10-156-761-2266

c 13	18.6	66.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 14	18.4	65.7	1443	13	US-10-042-991-11	Sequence 11, Appli
c 15	18.4	65.7	12305	18	US-10-422-323A-2	Sequence 2, Appli
c 16	18.4	65.7	12315	18	US-10-422-323A-1	Sequence 1, Appli
c 17	18.4	65.7	12980	9	US-09-238-076-5	Sequence 5, Appli
c 18	18.4	65.7	12980	10	US-09-995-937-5	Sequence 5, Appli
c 19	18.4	65.7	12980	10	US-09-917-563-5	Sequence 5, Appli
c 20	18.2	65.0	452	10	US-09-918-995-27460	Sequence 27460, A
c 21	18.2	65.0	2179	9	US-09-823-245A-434	Sequence 434, App
c 22	18.2	65.0	9875	10	US-09-764-891-7878	Sequence 7878, Ap
c 23	17.6	62.9	529	16	US-10-424-599-130933	Sequence 130933,
c 24	17.6	62.9	550	14	US-10-198-846-11819	Sequence 11819, A
c 25	17.6	62.9	838	14	US-10-198-846-3468	Sequence 3468, Ap
c 26	17.6	62.9	945	16	US-10-398-221-2508	Sequence 2508, Ap
c 27	17.6	62.9	945	16	US-10-398-221-2571	Sequence 2571, Ap
c 28	17.6	62.9	966	16	US-10-398-221-553	Sequence 553, App
c 29	17.6	62.9	966	16	US-10-398-221-554	Sequence 554, App
c 30	17.6	62.9	1646	16	US-10-282-122A-29374	Sequence 29374, A
c 31	17.6	62.9	9718	8	US-08-319-974A-1	Sequence 1, Appli
c 32	17.6	62.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c 33	17.6	62.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c 34	17.6	62.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
c 35	17.4	62.1	341	17	US-10-767-701-19049	Sequence 19049, A
c 36	17.4	62.1	379	10	US-09-738-269-20	Sequence 20, Appl
c 37	17.4	62.1	379	13	US-10-023-437-20	Sequence 20, Appl
c 38	17.4	62.1	382	17	US-10-437-963-17200	Sequence 17200, A
c 39	17.4	62.1	528	16	US-10-424-599-53946	Sequence 53946, A
c 40	17.4	62.1	558	13	US-10-027-632-237136	Sequence 237136,
c 41	17.4	62.1	558	15	US-10-027-632-237136	Sequence 237136,
c 42	17.4	62.1	589	18	US-10-363-345A-34197	Sequence 34197, A
c 43	17.4	62.1	589	18	US-10-363-345A-34198	Sequence 34198, A
c 44	17.4	62.1	691	18	US-10-363-345A-38631	Sequence 38631, A
c 45	17.4	62.1	691	18	US-10-363-345A-38631	Sequence 38631, A
c 46	17.4	62.1	774	16	US-10-282-122A-39862	Sequence 39862, A
c 47	17.4	62.1	778	16	US-10-282-122A-39862	Sequence 39862, A
c 48	17.4	62.1	983	13	US-10-011-033-11	Sequence 36749, A
c 49	17.4	62.1	2520	10	US-09-738-269-22	GENERAL INFORMA
c 50	17.4	62.1	2520	13	US-10-023-437-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-10-085-944-2
; Sequence 2, Application US/10085944
; Publication No. US20020155435A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Wei-Kung
; TITLE OF INVENTION: DETECTION OF DENGUE VIRUS
; FILE REFERENCE: 12563-004001
; CURRENT APPLICATION NUMBER: US/10/085,944
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/272,535
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-085-944-2

Query Match 100.0%; Score 28; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCAGAGAAACCGCG 28

Db 1 AATATGCTGAACGCAGAGAAACCGCG 28

```
RESULT 2
US-10-247-960-2
; Sequence 2, Application US/10247960
; Publication No. US20030175304A1
; GENERAL INFORMATION:
; APPLICANT: Hawaii Biotechnology Group, Inc.
; APPLICANT: Peters, Iain
; APPLICANT: Collier, Beth-Ann
; APPLICANT: McDonnell, Michael
; APPLICANT: Ivy, John
; APPLICANT: Harada, Kent
; TITLE OF INVENTION: RECOMBINANT DIMERIC ENVELOPE VACCINE
; FILE OF INVENTION: AGAINST FLAVIVIRAL INFECTION
; FILE REFERENCE: 24733-2005.01
; CURRENT APPLICATION NUMBER: US/10/247,960
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/376,463
; PRIOR FILING DATE: 1999-08-18
; PRIOR APPLICATION NUMBER: 08/904,227
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Dengue virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3381)
US-10-247-960-2

Query Match          100.0%; Score 28; DB 15; Length 3381;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 3
US-10-699-550-4
; Sequence 4, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 10724
; TYPE: DNA
; ORGANISM: Dengue virus type 2
US-10-699-550-4

Query Match          100.0%; Score 28; DB 18; Length 10724;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 40 AATATGCTGAAACGCGAGAGAAACCGCG 67

RESULT 4
US-10-699-550-3
; Sequence 3, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
; APPLICANT: WONG, SUSAN J.
; APPLICANT: SHI, PEI-YONG
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
; FILE REFERENCE: 454311-2232.1
; CURRENT APPLICATION NUMBER: US/10/699,550
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: 60/476,513
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 60/422,755
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/09036
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/402,860
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 60/281,947
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/275,025
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 10735
; TYPE: DNA
; ORGANISM: Dengue virus type 1
US-10-699-550-3

Query Match          94.3%; Score 26.4; DB 18; Length 10735;
Best Local Similarity 96.4%; Pred. No. 0.083;
Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
|||||
Db 134 AATATGCTGAAACGCGAGAGAAACCGCG 161

RESULT 5
US-09-840-707A-23
; Sequence 23, Application US/09840707A
; Patent No. US2002007276A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301C
; CURRENT APPLICATION NUMBER: US/09/840,707A
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
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US-09-840-707A-23

Query Match 92.9%; Score 26; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCG 26
|||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 6

US-10-038-557A-23
; Sequence 23, Application US/10038557A
; Publication No. US20030092684A1
; GENERAL INFORMATION:
; APPLICANT: Fredeking, Terry M.
; APPLICANT: Ignatyev, George M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS
; TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS
; FILE REFERENCE: 24881-301D
; CURRENT APPLICATION NUMBER: US/10/038,557A
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/840,707
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/562,979
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/198,210
; PRIOR FILING DATE: 1999-04-27
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: upper primer for Dengue virus type 2 detection
US-10-038-557A-23

Query Match 92.9%; Score 26; DB 14; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCG 26
|||||
Db 1 AATATGCTGAAACGCGAGAGAAACCG 26

RESULT 7

US-10-656-721-26
; Sequence 26, Application US/10656721
; Publication No. US20040265338A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Xiaowu
; APPLICANT: Dayton, Andrew I.
; APPLICANT: Zhang, Mingjie
; TITLE OF INVENTION: SUBGENOMIC REPLICONS OF THE FLAVIVIRUS
; TITLE OF INVENTION: DENGUE
; FILE REFERENCE: NIH202.001C1
; CURRENT APPLICATION NUMBER: US/10/656,721
; CURRENT FILING DATE: 2003-09-05
; PRIOR APPLICATION NUMBER: PCT/US02/06962
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/274,684
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 72
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: 5' primer
US-10-656-721-26

Query Match 78.6%; Score 22; DB 18; Length 72;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAA 22
|||||
Db 28 AATATGCTGAAACGCGAGAGAA 49

RESULT 8

US-10-425-115-108018
; Sequence 108018, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 108018
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MMT4577_30008C.1
US-10-425-115-108018

Query Match 70.0%; Score 19.6; DB 18; Length 594;
Best Local Similarity 84.6%; Pred. No. 67;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 27
|||||
Db 552 ATATGCTGATTACGAGAGAAACAGC 577

RESULT 9

US-10-363-345A-20593/c
; Sequence 20593, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 20593
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 20593
US-10-363-345A-20593

Query Match 67.9%; Score 19; DB 18; Length 765;
Best Local Similarity 81.5%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGC 28
|||||

Db 325 ATACGCCGAACGGCAACGAAAAACGCG 299

RESULT 10

US-10-363-345A-20594

; Sequence 20594, Application US/10363345A

; Publication No. US20040234960A1

; GENERAL INFORMATION:

; APPLICANT: Alexander Olek

; APPLICANT: Kurt Berlin

; TITLE OF INVENTION: Method for determining the degree of methylation of defined

; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3

; FILE REFERENCE: E01/1227

; CURRENT APPLICATION NUMBER: US/10/363,345A

; CURRENT FILING DATE: 2003-03-03

; NUMBER OF SEQ ID NOS: 40712

; SEQ ID NO 20594

; LENGTH: 765

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

; OTHER INFORMATION: CpG-island No: 20594

US-10-363-345A-20594

Query Match 67.9%; Score 19; DB 18; Length 765;

Best Local Similarity 81.5%; Pred. No. 1.3e+02;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGTAACGCGAGAGAACCGCG 28

|||||

Db 441 ATACGCCGAACGGCAACGAAAAACGCG 467

RESULT 11

US-10-369-493-32952/c

; Sequence 32952, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 32952

; LENGTH: 1428

; TYPE: DNA

; ORGANISM: Xylella fastidiosa

US-10-369-493-32952

Query Match 67.1%; Score 18.8; DB 15; Length 1428;

Best Local Similarity 90.9%; Pred. No. 1.7e+02;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CTGAACGCGAGAGAACCGCG 28

|||||

Db 1184 CGGAACCGCGAGAGAACCGCG 1163

RESULT 12

US-10-156-761-2266

; Sequence 2266, Application US/10156761

; Publication No. US20030119018A1

; GENERAL INFORMATION:


```
RESULT 14
US-10-042-991-11
; Sequence 11, Application US/10042991
; Publication No. US2002012407A1
; GENERAL INFORMATION:
; APPLICANT: Ian M. Whitehead
; APPLICANT: Alan Slusarenko
; APPLICANT: Duncan Gaskin
; APPLICANT: Alan Brash
; APPLICANT: Nathalie Tijet
; TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
; FILE REFERENCE: 06027.0001U3
; CURRENT APPLICATION NUMBER: US/10/042,991
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Capsicum annuum (green pepper)
US-10-042-991-11

Query Match      65.7%; Score 18.4; DB 13; Length 1443;
Best Local Similarity 78.6%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 933 AATATGCTGAGATGCAAGAGAAACTGAG 960

RESULT 15
US-10-422-323A-2/c
; Sequence 2, Application US/10422323A
; Publication No. US20040214178A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER, INC.
; TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
; FILE REFERENCE: PC19102A (AG0190)
; CURRENT APPLICATION NUMBER: US/10/422,323A
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 60/375,667
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/375,667
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 12305
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicati
US-10-422-323A-2

Query Match      65.7%; Score 18.4; DB 18; Length 12305;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 9039 AATATGCTAAACGCGCATACCCCGCG 9012

RESULT 16
US-10-422-323A-1/c
; Sequence 1, Application US/10422323A
; Publication No. US20040214178A1
; GENERAL INFORMATION:
; APPLICANT: PFIZER, INC.
```

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; TITLE OF INVENTION: REPORTER-SELECTABLE HEPATITIS C VIRUS REPLICON
; FILE REFERENCE: PC19102A (AG0190)
; CURRENT APPLICATION NUMBER: US/10/422,323A
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: 60/375,667
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/375,667
; PRIOR FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12315
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A cell line wherein the nucleic acid molecule is a self replicati
US-10-422-323A-1

Query Match      65.7%; Score 18.4; DB 18; Length 12315;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAAACGCGAGAGAAACCGCG 28
Db 9209 AATATGCTAAACGCGCATACCCCGCG 9182

RESULT 17
US-09-238-076-5/c
; Sequence 5, Application US/09238076
; Patent No. US20020102540A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAPERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/238,076
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/034,756
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-238-076-5
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Query Match      65.7%; Score 18.4; DB 9; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 18
US-09-995-937-5/c
; Sequence 5, Application US/09995937
; Publication No. US20030028010A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,937
; FILING DATE: 28-May-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/034,756
; FILING DATE: 04-May-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-995-937-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 19
US-09-917-563-5/c
; Sequence 5, Application US/09917563
; Publication No. US20030073080A1
; GENERAL INFORMATION:
; APPLICANT: RICE, CHARLES et al.
; TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C

```

```

; VIRUS (HCV) AND USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,563
; FILING DATE: 27-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/238,076
; FILING DATE: 26-JAN-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 6029-4831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-917-563-5

Query Match      65.7%; Score 18.4; DB 10; Length 12980;
Best Local Similarity 78.6%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGGAGAGAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 9714 AATATGCTAAACGCGGCATACCCCGCG 9687

RESULT 20
US-09-918-995-27460
; Sequence 27460, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27460
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-27460

```

Qy 1 AATATGCTGAACCGGAGAGAAA 23
Db 636 AAGATGCTGAACAGGAGAGAAA 614

QY 1 AAATATGCTGAAACGCGAGAGAAAC 24

```

RESULT 29
US-10-398-221-554
; Sequence 554, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US

```

; TYPE: DNA
 ; ORGANISM: *Neisseria meningitidis*
 US-10-282-122A-29374

```

/ GENERAL INFORMATION:
/ APPLICANT: KUNST, Frederik
/ APPLICANT: GLASER, Philippe
/ TITLE OF INVENTION: Liscerta innocua, genome and applications
/ FILE REFERENCE: 344 702 - US
/ CURRENT APPLICATION NUMBER: US/10/398,221
/ CURRENT FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
/ PRIOR FILING DATE: 2001-10-04

```

Query Match 62.9%; Score 17.6; DB 16; Length 3011208;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Query Match      62.9%; Score 17.6; DB 16; Length 3011208;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 20: Conservative 0; Mismatches 4; Indels 0; G
```

QY
3 TATGCTGAAACGCGAGAGAAAAACCG 26
|||||
pb
2434485 TATGCTGAAACACATGAGAAAAACAG 24

RESULT 35

```
Query Match      62.1%; Score 17.4; DB 17; Length 341;
Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21: Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
Dp 335 AAAAGGGTAAACACGGAGAGAAACCGC 309

RESULT 36

/ APPLICANT: JOHNSTON, STEPHEN A.
 / APPLICANT: STEMKE-HALE, KATHERINE
 / APPLICANT: SYKES, KATHRYN F.
 / APPLICANT: KALTENBOECK, BERNHARD
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
 / NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
 / TITLE OF INVENTION: CHLAMYDIA PSITTACI
 / FILE REFERENCE: UTSD:659
 / CURRENT APPLICATION NUMBER: US/09/738,269
 / CURRENT FILING DATE: 2000-12-18
 / NUMBER OF SEQ ID NOS: 61
 / SOFTWARE: Patent In Ver. 2.1

US-09-738-269-20

Query Match 62.1%; Score 17.4; DB 10; Length 379;

Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
|||||
Db 59 ATATGCTGATAATAGAGAGAACCTGCG 33

RESULT 37

US-10-023-437-20/c
; Sequence 20, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEKKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD-736US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-20

Query Match 62.1%; Score 17.4; DB 13; Length 379;
Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
|||||
Db 59 ATATGCTGATAATAGAGAGAACCTGCG 33

RESULT 38

US-10-437-963-17200
; Sequence 17200, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 17200
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(382)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22877C.1
US-10-437-963-17200

Query Match 62.1%; Score 17.4; DB 17; Length 382;

Best Local Similarity 77.8%; Pred. No. 6.2e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
|||||
Db 79 AATTGTGGAAGCGGACAAAACCCAC 105

RESULT 39

US-10-424-599-53946/c
; Sequence 53946, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 53946
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19726C.1
US-10-424-599-53946

Query Match 62.1%; Score 17.4; DB 16; Length 528;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
|||||
Db 294 ATATCCAAAACGCGAGAGAGCAGCG 268

RESULT 40

US-10-027-632-237136/c
; Sequence 237136, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237136
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature

```
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136

Query Match      62.1%; Score 17.4; DB 13; Length 558;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 263 AATATGCTGAAGAGGGATATAAACCGC 237

RESULT 41
US-10-027-632-237136/c
; Sequence 237136, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237136
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(558)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-237136

Query Match      62.1%; Score 17.4; DB 15; Length 558;
Best Local Similarity 77.8%; Pred. No. 6.5e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 263 AATATGCTGAAGAGGGATATAAACCGC 237

RESULT 42
US-10-363-345A-34197/c
; Sequence 34197, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 263 AATATGCTGAAGAGGGATATAAACCGC 237

RESULT 43
US-10-363-345A-34198
; Sequence 34198, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 34198
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 34198
US-10-363-345A-34198

Query Match      62.1%; Score 17.4; DB 18; Length 589;
Best Local Similarity 77.8%; Pred. No. 6.6e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
    |||  ||||| ||||| ||||| |||||
Db 166 ATACCGCGAAACGCGAAAAAAACCGCG 140

RESULT 44
US-10-363-345A-38631/c
; Sequence 38631, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 38631
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 38631
US-10-363-345A-38631
```



```
Query Match          62.1%; Score 17.4; DB 18; Length 691;
Best Local Similarity 77.8%; Pred. No. 6.7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGCAGAGAAACCGC 28
    ||| | ||||| ||| ||||| |||
Db 226 ATAAACCGAACTCGAAAAAACCGC 200

RESULT 45
US-10-363-345A-38632
; Sequence 38632, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 38632
; LENGTH: 691
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 38632
US-10-363-345A-38632

Query Match          62.1%; Score 17.4; DB 18; Length 691;
Best Local Similarity 77.8%; Pred. No. 6.7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGCAGAGAAACCGC 28
    ||| | ||||| ||| ||||| |||
Db 466 ATAAACCGAACTCGAAAAAACCGC 492

RESULT 46
US-10-282-122A-39862/c
; Sequence 39862, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36749
; LENGTH: 778
```

```
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39862
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Salmonella typhi
US-10-282-122A-39862

Query Match          62.1%; Score 17.4; DB 16; Length 774;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGGCAGAGAAACCGC 27
    ||| | ||||| ||| ||||| |||
Db 528 AATACGCTGAACGGCAGAGATAAATCGC 502

RESULT 47
US-10-282-122A-36749/c
; Sequence 36749, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36749
; LENGTH: 778
```

```
; TYPE: DNA
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-36749

Query Match          62.1%; Score 17.4; DB 16; Length 778;
Best Local Similarity 77.8%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAGAAACCGC 27
    ||||| ||||| ||||| ||||| |||||
Db 525 AATACGCTGAACGCGAGAGATTAATCGC 499

RESULT 48
US-10-011-033-11
; GENERAL INFORMATION:
; APPLICANT: Boeshore, Maury L
; McMaster, J. Russell
; Tricoli, David M
; Reynolds, John F
; Carney, Kim J
; TITLE OF INVENTION: Plants Resistant to C Strains of
; Cucumber Mosaic Virus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rocky, Milnamow & Katz, Ltd.
; STREET: 2 Prudential Plaza, 180 N. Stetson, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60089
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,033
; FILING DATE: 13-No. US20020124286A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,233
; FILING DATE: 26-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lisa V. Mueller
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; JOURNAL: J. Gen. Virol.
; VOLUME: 70
; PAGES: 1065-1073
; DATE: 1989
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-011-033-11
```

```
Query Match          62.1%; Score 17.4; DB 13; Length 983;
Best Local Similarity 77.8%; Pred. No. 7e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 113 AGATGCTGAAACTCAATAGAACCTCG 139
```

```
RESULT 49
US-09-738-269-22/c
; Sequence 22, Application US/09738269
; Publication No. US20030185849A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
```

```
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22
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Query Match          62.1%; Score 17.4; DB 10; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 1856 ATATGCTGATAATAGAGAACCTGCG 1830
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RESULT 50
US-10-023-437-22/c
; Sequence 22, Application US/10023437
; Publication No. US20020183272A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
; AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
; FILE REFERENCE: UTSD:738US
; CURRENT APPLICATION NUMBER: US/10/023,437
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/225,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-10-023-437-22
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Query Match          62.1%; Score 17.4; DB 13; Length 2520;
Best Local Similarity 77.8%; Pred. No. 7.8e+02;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ATATGCTGAAACGCGAGAGAAACCGCG 28
    ||||| ||||| ||||| ||||| |||||
Db 1856 ATATGCTGATAATAGAGAACCTGCG 1830
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Search completed: January 19, 2005, 13:58:54
Job time : 223 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 19, 2005, 12:51:42 ; Search time 1550 Seconds
(without alignments)
658.266 Million cell updates/sec

Title: US-10-085-944-2

Perfect score: 28

Sequence: 1 aatatgtgaacgcgagagaaccgcg 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	20.6	73.6	776	7	CF996467
c 2	19.8	70.7	720	7	CF455745
c 3	19.6	70.0	301	6	CB078143
c 4	19.6	70.0	712	7	CF372439
c 5	19.6	70.0	722	7	CF512147
c 6	19.6	70.0	734	7	CF512236
c 7	19.4	69.3	464	2	BE841207
c 8	19	67.9	520	9	CR305770
c 9	19	67.9	559	9	TA262H01Q
c 10	19	67.9	568	8	AQ945692
c 11	19	67.9	576	9	TA140D12P
c 12	19	67.9	580	2	BE776235
c 13	19	67.9	602	1	AL673619
c 14	19	67.9	629	1	AL647632
c 15	19	67.9	633	6	CA349616
c 16	19	67.9	649	6	CA356841
c 17	19	67.9	738	9	AG363192
c 18	19	67.9	768	9	CC504335
c 19	19	67.9	870	9	AG186531
c 20	19	67.9	988	7	CF995511
c 21	18.8	67.1	1687	2	BF128456
c 22	18.6	66.4	407	6	CF198531
c 23	18.6	66.4	456	4	BG659286
c 24	18.6	66.4	563	7	CF939381

25	18.6	66.4	584	8	AQ657703
26	18.6	66.4	593	9	FR0021761
c 27	18.6	66.4	636	7	CO300868
28	18.6	66.4	640	7	CN876173
29	18.6	66.4	642	1	AI135620
30	18.6	66.4	671	7	CN882707
31	18.6	66.4	675	7	CN879811
32	18.6	66.4	683	7	CN918097
c 33	18.6	66.4	684	8	AQ657387
34	18.6	66.4	799	9	CL527496
c 35	18.4	65.7	427	9	CG016439
c 36	18.4	65.7	456	8	AQ724090
c 37	18.4	65.7	496	2	AW599272
c 38	18.4	65.7	582	8	BZ130571
c 39	18.4	65.7	655	6	CB020289
c 40	18.4	65.7	672	8	BH100535
c 41	18.4	65.7	675	6	CA112278
c 42	18.4	65.7	695	8	BH929269
c 43	18.4	65.7	697	8	BH549312
c 44	18.4	65.7	743	7	CK326303
c 45	18.4	65.7	750	2	BB615972
c 46	18.4	65.7	774	8	BZ154086
c 47	18.4	65.7	788	8	BZ132164
c 48	18.4	65.7	790	2	BF678988
c 49	18.4	65.7	792	4	BI753870
c 50	18.4	65.7	824	2	BF620613

ALIGNMENTS

RESULT 1
CF996467/c

LOCUS

DEFINITION AGENCOURT 16394292 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7037741
5' mRNA sequence.

ACCESSION CF996467

VERSION CF996467.1

KEYWORDS GI:38517318

SOURCE EST.

ORGANISM Danio rerio (zebrafish)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 776)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue procurement: Len Zon, Harvard

cDNA Library Preparation: Open Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:

<http://image.llnl.gov>

Plate: LIAM14788 row: e column: 03

High quality sequence stop: 734.

Location/Qualifiers

1..776

/organism="Danio rerio"

/mol_type="mRNA"

/db_xref="taxon:7955"

/clone="IMAGE:7037741"

/tissue_type="whole body"

/lab_host="DH10B"

/clone_lib="NIH_ZGC_7"

/note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;

Bulk tissue was collected from a whole adult individual

TITLE Expressed sequence tags from the grapevine cultivar Cabernet Sauvignon
JOURNAL Unpublished (2003)
COMMENT Contact: Mark R. Thomas
 CSIRO Plant Industry
 CSIRO
 PO Box 350, Glen Osmond, SA, 5064, Australia
 Tel: 61 8 83038600
 Fax: 61 8 83038601
 Email: Mark.R.Thomas@csiro.au
 Seq primer: CCCAGTCACGACGTGTAAACG (M13 Forward)
 POLYA=Yes.

FEATURES

Location/Qualifiers

1..712

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CSRS052D08"

/sex="Hermaphrodite"

/dev_stage="12 - modified E-L system"

/clone_lib="CabSau Normalised Flower Stage 12 (FL0n0012)"

/note="Organ: Inflorescence including flowers; Vector:

pZL; Normalised cDNA library from immature inflorescences at stage 12 of the modified E-L system. Tissue collected from field grown plants. A description of the modified E-L system can be found in the paper by B. G. Coombe 'Adoption of a system for identifying grapevine growth stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."

ORIGIN

Query Match 70.0%; Score 19.6; DB 7; Length 712;

Best Local Similarity 84.6%; Pred. NO. 3.9e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAAACCG 26

Db 374 ATTATGCTGAAACTCGAAGAAACTG 399

RESULT 5

CF512147/c

LOCUS CF512147 722 bp mRNA linear EST 09-SEP-2003
DEFINITION CABud0003_IF_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
 Bud - CABUD Vitis vinifera cDNA clone CABud0003_IF_A10 5', mRNA sequence.

ACCESSION CF512147**VERSION** CF512147.1 GI:34543915**KEYWORDS** EST.**SOURCE** Vitis vinifera**ORGANISM** Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 722)**AUTHORS** Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.**TITLE** Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'

berries at various developmental stages

JOURNAL Unpublished (2003)**COMMENT** Contact: Douglas Cook, PhD

CAES Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: drcook@ucdavis.edu

Seq primer: ACGGACCGACATATGCC.

Location/Qualifiers

1..722

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon (Clone 8)"

/db_xref="taxon:29760"

/clone="CABud0003_IF_A10"

/sex="Hermaphrodite"

/dev_stage="Pre-bloom (10-11 days before bloom)"

/lab_host="DHSalpa"

/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"

/note="Organ: Bud; Vector: pDNR; Site 1: SfiI; Site 2:

SfiI; CABUD is a cDNA library of Vitis vinifera cv.

'Cabernet Sauvignon' Clone 8 dissected buds. Samples were

collected May 13, 2002 from pre-bloom plants (10-11 days

before bloom), pre-veraison. Sampled vines were located at

the University of California, Davis, Experimental

Vineyard. cDNAs were made by oligo-dT priming and

directionally cloned. 5' and 3' adaptors were used in

cloning as follows:

5'-AAGCAGTGTATCAACGAGAGTGGCCATTACGGCCGG-3' and

5'-ATTCTAGGCGGCGCGCATG-DT(30)NN-3'. Library was

constructed using the Clontech Creator SMART kit and

size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 70.0%; Score 19.6; DB 7; Length 722;

Best Local Similarity 84.6%; Pred. NO. 3.9e+02;

Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAAACGCGAGAAACCG 26

Db 350 ACTATGCTGAAACTCGAAGAAACTG 325

RESULT 6

CF512236

LOCUS

DEFINITION CF512236 734 bp mRNA linear EST 09-SEP-2003
 CABud0003_IR_A10 Vitis vinifera cv. cabernet sauvignon (Clone 8)
 Bud - CABUD Vitis vinifera cDNA clone CABud0003_IR_A10 3', mRNA sequence.

ACCESSION CF512236**VERSION** CF512236.1 GI:34544004**KEYWORDS** EST.**SOURCE** Vitis vinifera**ORGANISM** Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.

REFERENCE 1 (bases 1 to 734)**AUTHORS** Jones, K. and Cook, D.

Goes da Silva, F., Iandolino, A., Lim, H., Baek, J., Leslie, A., Xu, J., Jones, K. and Cook, D.

TITLE Expressed sequence tags from Vitis vinifera 'Cabernet Sauvignon'

berries at various developmental stages

JOURNAL Unpublished (2003)**COMMENT** Contact: Douglas Cook, PhD

CAES Genome Facility

UC Davis, Plant Pathology

One Shields Ave, Davis, CA 95616, USA

Tel: 530 754 6561

Fax: 530 754 6617

Email: drcook@ucdavis.edu

Seq primer: GCCAACCAGATGCTAG.

Location/Qualifiers

1..734

/organism="Vitis vinifera"

/mol_type="mRNA"

/cultivar="Cabernet Sauvignon (Clone 8)"

/db_xref="taxon:29760"

/clone="CABud0003_IR_A10"

/sex="Hermaphrodite"

/dev_stage="Pre-bloom (10-11 days before bloom)"

/lab_host="DHSalpa"

/clone_lib="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"

/note="Organ: Bud; Vector: pDNR; Site 1: SfiI; Site 2:

SfiI; CABUD is a cDNA library of Vitis vinifera cv.

'Cabernet Sauvignon' Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
 5'-AAGCAGTGGTATCAACGACGAGTGGCCATTTACGCCGGG-3' and
 5'-ATTCTAGAGCGGCGCGGCATG-DT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 70.0%; Score 19.6; DB 7; Length 734;
 Best Local Similarity 84.6%; Pred. No. 3.9e+02;
 Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCG 26
 Db 373 ACTATGCTGAACGCGAGAGAAACCG 398

RESULT 7

BE841207/c
 LOCUS BE841207 464 bp mRNA linear EST 22-SEP-2000
 DEFINITION QV4-SN0024-200700-304-a07 SN0024 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE841207
 VERSION BE841207.1 GI:10273585
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 464)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bata G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-QV4-SN0024-200700-304-a07&tl3=2000-07-20&tl4=1)

Seq primer: puc 18 forward

High quality sequence start: 10

High quality sequence stop: 248.

FEATURES

source

1. .464
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="SN0024"
 /note="Organ: stomach normal; Vector: puc18; Site:1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Query Match 69.3%; Score 19.4; DB 2; Length 464;
 Best Local Similarity 95.2%; Pred. No. 4.6e+02;
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 TGCTGAACGCGAGAGAAACC 25
 Db 329 TGCTGAACGCGAGAGAAACC 309

ORIGIN

RESULT 8
 CR305770
 LOCUS CR305770 520 bp DNA linear GSS 01-MAR-2004
 DEFINITION Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.

ACCESSION CR305770

VERSION CR305770.1 GI:44851914

KEYWORDS GSS.

SOURCE Medicago truncatula (barrel medic)

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

REFERENCE 1 (bases 1 to 520)

Genoscope.

Direct Submission

TITLE

JOURNAL

Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage ;
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr

FEATURES

source

1. .520
 /location/Qualifiers
 /organism="Medicago truncatula"
 /mol_type="genomic DNA"
 /cultivar="Jemalong A17"
 /db_xref="taxon:3880"
 /clone_lib="MTE1"
 /note="Vector: pindigobac ; Site 1: EcoRI ; Site 2: EcoRI ; Debelle F. and Chalhou B.-Genoscope sequence ID : mte1-25N13RM1"

ORIGIN

Query Match 67.9%; Score 19; DB 9; Length 520;
 Best Local Similarity 81.5%; Pred. No. 7.1e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCG 27
 Db 241 AACAGGCTGCAACGCGAGAGAAACCG 267

RESULT 9

TA262H01Q

LOCUS TA262H01Q 559 bp DNA linear GSS 13-DEC-2000

DEFINITION T. brucei sheared genomic DNA clone 262h01, reverse sequence, genomic survey sequence.

ACCESSION AL487728

VERSION AL487728.1 GI:11850764

KEYWORDS GSS.

SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei

Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma

1 (bases 1 to 559)

REFERENCE

AUTHORS

Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R., Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L., Melville S.E., Rajadream M.A. and Barrell B.G.

Direct Submission

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The *v* + *i* method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

Query Match	67.9%	Score 19;	DB 8;	Length 568;
Best Local Similarity	81.5%;	Pred. No. 7.1e+02;		
Matches 22;	Conservative	0;	Mismatches 5;	Indels
				0;
				Gaps 0;

RESULT 11					
TA140D12P					
LOCUS	TA140D12P	576 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	T. brucei sheared genomic DNA clone 140D12, forward sequence, genomic survey sequence.				

REFERENCE
AUTHORS
TITLE
JOURNAL

1-7 (bases 1 to 576)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Akin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

COMMENT

ms@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The $v + i$ method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.

Query Match	67.9%	Score 19;	DB 9;	Length 576;
Best Local Similarity	81.5%;	Pred. No. 7.1e+02;		
Matches 22: Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0;

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/clone_id="Sheared DNA"
/note="Vector: pUC18; Site 1: SmaI; Constructed at The

```



```

/lab host="Escherichia coli XLI-blue"
/clone lib="XGC-gastrula"
/note="Vector: pGS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pGS107 with EcoRI at the 5' end and NotI at the 3'
end."

ORIGIN
Query Match      67.9%; Score 19; DB 1; Length 629;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAAACCGC 28
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 234 ATAACTGAAAGCGAGAGAAACGTG 260

RESULT 15
CA349616
LOCUS
DEFINITION 633 bp mRNA linear EST 05-NOV-2002
5', mRNA sequence.
ACCESSION CA349616
VERSION CA349616.1 GI:24594787
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 633)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGATAACAATTTCACACGAG.
FEATURES
Location/Qualifiers
source
1..633
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="IRT142M04_C G02"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="NCCWA IRT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN
Query Match      67.9%; Score 19; DB 6; Length 633;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 579 AATATGCAAACTCGAGAGAAAGCTGC 605

RESULT 16
CA356841
LOCUS
DEFINITION 649 bp mRNA linear EST 05-NOV-2002
5', mRNA sequence.
ACCESSION CA356841
VERSION CA356841.1 GI:24602028
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 649)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGATAACAATTTCACACGAG.
FEATURES
Location/Qualifiers
source
1..649
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="IRT100M13_A G07"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="NCCWA IRT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN
Query Match      67.9%; Score 19; DB 6; Length 649;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 AATATGCAGAACTCGAGAGAAAGCTGC 495

RESULT 17
AG363192/c
LOCUS
DEFINITION 738 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-164N14.TJ, genomic survey
sequence.
ACCESSION AG363192
VERSION AG363192.1 GI:47974397
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 738)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
REFERENCE
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@igsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

```

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629106 NCCWA IRT Oncorhynchus mykiss cDNA clone IRT100M13_A_G07
5', mRNA sequence.
ACCESSION CA356841
VERSION CA356841.1 GI:24602028
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 649)
Rexroad, C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G.,
Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of a
gene index
CytoGenet. Genome Res. 102 (1-4), 347-354 (2003)
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WV 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@nccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by
cross_match v0.990329.
Seq primer: AGCGATAACAATTTCACACGAG.
FEATURES
Location/Qualifiers
source
1..649
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="IRT100M13_A G07"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="NCCWA IRT"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from brain, gill, liver,
spleen, muscle, and kidney."

ORIGIN
Query Match      67.9%; Score 19; DB 6; Length 649;
Best Local Similarity 81.5%; Pred. No. 7.2e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGC 27
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 AATATGCAGAACTCGAGAGAAAGCTGC 495

RESULT 17
AG363192/c
LOCUS
DEFINITION 738 bp DNA linear GSS 03-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-164N14.TJ, genomic survey
sequence.
ACCESSION AG363192
VERSION AG363192.1 GI:47974397
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 738)
Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submission
REFERENCE
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: hattori@igsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)

```

Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
 phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@rtc.riken.jp

PRIMERS
 Sequencing : TJ
 LIBRARY
 Vector : DBACe3.6
 R.Site 1 : ECORI
 R.Site 2 : ECORI.

FEATURES
 source
 1..738
 Location/Qualifiers
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSNg01-164N14.TJ"
 /sex="male"
 /tissue_type="mixture of kidney and spleen"
 /clone_lib="MSNg01 Mouse Male BAC Library"

ORIGIN
 Query Match 67.9%; Score 19; DB 9; Length 738;
 Best Local Similarity 81.5%; Pred. No. 7.3e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACCGGAGAGAAACCGC 27
 ||||| ||||| ||||| ||||| |||||
 Db 690 AATATACCGAAAGCGAGGAAAGCGC 664

RESULT 18
 CC504335
 LOCUS
 DEFINITION
 CC504335 768 bp DNA linear GSS 17-JUN-2003
 CH240_344G2.T7 CHORI-240 Bos taurus genomic clone CH240_344G2,
 genomic survey sequence.
 CC504335
 CC504335.1 GI:31822628
 GSS.
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 768)
 Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
 Tsai,M., Cloutier,A., Lee,D., Girm,N., Olson,T., Mayo,M.,
 Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
 Mathewson,C., Wye,N., Mason,A., Brown-John,M., Jones,S.,
 Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
 Dalrymple,B.P. and Tellam,R.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 Unpublished (2003)
 Other_GSSs: CH240_344G2.TARBAC13P2
 Contact: Rob Holt
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccsc.ca
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering_information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.
 Plate: 344 row: G column: 2

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Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 690 ATATGCGAATCGCGAGAGAACCGCG 664

RESULT 20
CF995511/c
LOCUS CF995511 988 bp mRNA linear EST 25-NOV-2003
DEFINITION AGNCOURT 16028690 NIH MGC 217 Homo sapiens cDNA clone
IMAGE:30524078 5', mRNA sequence.
ACCESSION CF995511
VERSION CF995511.1 GI:38512120
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM603 row: a column: 15
High quality sequence stop: 407.
Location/Qualifiers
1..988
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30524078"
/tissue type="Pooled Chondrosarcoma Tumor cells"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NIH MGC 217"
/note="Vector: pYX-Asc; Site 1: EcoRI; Site 2: NotI;
Library is oligo-dT primed and directionally cloned.
Denatured RNA was size fractionated on a 1% agarose gel.
First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGCGACGAG)3' and 5'd
(CCTGCTGCGG)3'. 3' Linker sequence - CGCGCGCTGAGAGCC T18.
Sequencing primers 3'end: T3 promoter primer 5'd
(ATTAAACCTCACTAAAGGA)3', 5' End: T7 promoter primer 5'd
(TAATACACCTCACTATAGG)3'. Average insert size 0.5-1kb.
Library was constructed in the laboratory of M. Bento
Soares. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 67.9%; Score 19; DB 7; Length 988;
Best Local Similarity 81.5%; Pred. No. 7.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAACCGCG 27
||||| ||||| ||||| ||||| |||||
Db 727 ATTATGCGAATCGCGAGAGAACCGCG 701

Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 ATATGCTGAACGCGAGAGAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 690 ATATGCGAATCGCGAGAGAACCGCG 664

RESULT 21
BF128456
LOCUS BF128456 1687 bp mRNA linear EST 24-OCT-2000
DEFINITION 601810142R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053059 3',
mRNA sequence.
ACCESSION BF128456
VERSION BF128456.1 GI:10967496
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1687)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM891 row: c column: 12
High quality sequence start: 26
High quality sequence stop: 165.
Location/Qualifiers
1..1687
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4053059"
/tissue type="leiomyosarcoma cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 67.1%; Score 18.8; DB 2; Length 1687;
Best Local Similarity 90.9%; Pred. No. 9.4e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CTGAACGCGAGAGAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 694 CAGACACGCGAGAGAACCGCG 715

RESULT 22
CF198531/c
LOCUS CF198531 407 bp mRNA linear EST 01-AUG-2003
DEFINITION EST0126 Tamarix androssowii leaf Tamarix androssowii cDNA, mRNA
sequence.
ACCESSION CF198531
VERSION CF198531.1 GI:33392904
KEYWORDS EST.
SOURCE Tamarix androssowii
ORGANISM Tamarix androssowii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Tamaricaceae; Tamarix.
REFERENCE 1 (bases 1 to 407)
AUTHORS Wang, Y., Yang, C., Jiang, J., Liu, G., Wu, J. and Liu, Z.
TITLE EST acquired from cDNA library of Tamarix androssowii treated with

```

NaHCO₃
 Unpublished (2003)
 Contact: Yucheng Wang
 Forestry Source and Environment College
 Northeast Forestry University
 Hexing 26, Harbin, Heilongjiang, 150040, P.R. China
 Tel: 086-451-2190607
 Email: WANGYUCHENG1029@YAHOO.COM.CN.

FEATURES
 source
 1. .407
 /organism="Tamarix androssowii"
 /mol_type="mRNA"
 /db_xref="taxon:189785"
 /tissue_type="leaf"
 /clone_lib="Tamarix androssowii leaf"

ORIGIN
 Query Match 66.4%; Score 18.6; DB 6; Length 407;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AATATGCTGAACGCGAGAGAAACC 25
 ||||| ||||| ||||| ||||| |||||
 Db 328 AATATGCTTGAAGGAGAGAAACC 304
 ||||| ||||| ||||| ||||| |||||

RESULT 23
 BG659286/c
 LOCUS
 DEFINITION TGSTzya21d01.y1 TgVEG118 Tachyzoite cDNA Library Toxoplasma gondii
 cDNA clone TGESTzya21d01.y1 5' similar to TR:081505 O81505 F9D12.1
 PROTEIN. i, mRNA sequence.

ACCESSION BG659286
 VERSION BG659286.1 GI:13801535
 KEYWORDS EST.
 SOURCE Toxoplasma gondii
 ORGANISM Toxoplasma gondii
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Toxoplasma.
 1 (bases 1 to 456)
 Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioke, J.A., White, M., Clifton, S., Pape, D., Martin, J., Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.
 Toxoplasma EST Project
 Unpublished (2001)
 Contact: Clifton, S.
 Toxoplasma EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: toxo@watson.wustl.edu
 Contact David Sibley (toxoeest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
 Seq primer: -40RP from Gibco
 High quality sequence stop: 408.

FEATURES
 source
 1. .456
 /organism="Toxoplasma gondii"
 /mol_type="mRNA"
 /strain="VEG"
 /db_xref="taxon:5811"
 /clones="TGESTzya21d01.y1"
 /dev_stage="Tachyzoite"
 /lab_host="DH10B"
 /clone_lib="TGVEG118 Tachyzoite cDNA Library"
 /note="Vector: pBluescript SK; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Kelian Tang, Robert Cole, and L. David Sibley at Washington University. cDNAs were synthesized from poly(A)+ RNA by oligo(dT) priming, size-selected and directionally cloned into the Uni-ZAP XR

lambda vector (Stratagene). The primary library was mass excised as phagemids and rescued in SOLR cells. The plasmid library was recovered from the SOLR cells and transformed in mass into DH10B (GeneHog, Research Genetics, Inc.) for sequencing. WARNING: This library may contain a small percentage contaminants from human fibroblast cells."

ORIGIN
 Query Match 66.4%; Score 18.6; DB 4; Length 456;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 ATATGCTGAACGCGAGAGAAACC 26
 ||||| ||||| ||||| ||||| |||||
 Db 435 ATATCTGMAATGCGAGATACAG 411
 ||||| ||||| ||||| ||||| |||||

RESULT 24
 CF939381/c
 LOCUS
 DEFINITION NCSTGabs7g05.y1 Nc-1 Tachyzoite cDNA Library 2 Neospora caninum
 cDNA 5' similar to SW:YC27_HUMAN Q9Y316 HYPOTHETICAL PROTEIN
 CGI-27, mRNA sequence.

ACCESSION CF939381
 VERSION CF939381.1 GI:38438622
 KEYWORDS EST.
 SOURCE Neospora caninum
 ORGANISM Neospora caninum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Sarcocystidae; Neospora.
 1 (bases 1 to 563)
 Cole, R., Fogarty, S., Tang, K., Howe, D.K., Sibley, L.D., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wyllie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R., Fedele, M., Belaygorod, L., Franklin, C., Carri, L.M., Grow, A., Maguire, L., Wadkins, J., Richey, J., Waterston, R. and Wilson, R.
 USDA-WashU Neospora EST Project
 Unpublished (2000)
 Contact: Sandy Clifton, Ph.D. - Neospora
 USDA-WashU Neospora EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Contact David Sibley (toxoeest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1. .563
 /organism="Neospora caninum"
 /mol_type="mRNA"
 /db_xref="taxon:29176"
 /dev_stage="Tachyzoite"
 /lab_host="GC10 Competent Cells(PGC)"
 /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by Kelian Tang, and Robert Cole at Washington University. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and electroporated into GC10 Competent Cells(PGC). The library may contain a small percentage of host or bacterial contaminants."

FEATURES
 source
 1. .563
 /organism="Neospora caninum"
 /mol_type="mRNA"
 /db_xref="taxon:29176"
 /dev_stage="Tachyzoite"
 /lab_host="GC10 Competent Cells(PGC)"
 /clone_lib="Nc-1 Tachyzoite cDNA Library 2"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed by Kelian Tang, and Robert Cole at Washington University. cDNA was synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and electroporated into GC10 Competent Cells(PGC). The library may contain a small percentage of host or bacterial contaminants."

ORIGIN
 Query Match 66.4%; Score 18.6; DB 7; Length 563;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;


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Plate: EK.1795 row: E column: 4
High quality sequence stop: 467.
Location/Qualifiers
1. .636
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="EK179552"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site 1: NotI; Site 2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."

ORIGIN
Query Match 66.4%; Score 18.6; DB 7; Length 636;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGCAGAGAAACCG 26
||||| ||||||| ||||||| |||
Db 205 ATATGCTGAACGGCAGAGAAACCG 181

RESULT 28
CN876173 640 bp mRNA linear EST 04-JUN-2004
LOCUS 020813AARA008897HT (AARA) Royal Gala partially senescing leaf Malus
DEFINITION x domestica cDNA clone AARA008897, mRNA sequence.
ACCESSION CN876173
VERSION CN876173.1 GI:48262413
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 640)
/clone_lib="AARA008897"
/dev_stage="adult"
/lab_host="DHS - alpha"
/note="Organ: head; Vector: pOT2; Site 1: EcoRI; Site 2:
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.
Location/Qualifiers
1. .640
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AARA008897"
/tissue_type="Leaf"
/dev_stage="Partially senescing leaf"
/clone_lib="(AARA) Royal Gala partially senescing leaf"
/note="Vector: pBK-CMV; Library sequenced by Genesis
Research & Development"

ORIGIN
Query Match 66.4%; Score 18.6; DB 7; Length 640;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGCAGAGAAACCG 26
||||| ||||||| ||||||| |||
Db 43 ATATCCTGAACGGCAGAGACGCTG 67

RESULT 29
A1135620 642 bp mRNA linear EST 02-DEC-2003
LOCUS GH13441.5prime GH Drosophila melanogaster head pOT2 Drosophila
DEFINITION melanogaster cDNA clone GH13441 5 similar to CG9322: FBan0009322
GO: [] located on: 3R 87F12-87F12; 08/12/2002, mRNA sequence.
ACCESSION A1135620
VERSION A1135620.1 GI:3628178
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 642)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HMMI Drosophila EST Project
Unpublished (2001)
Other_ESTs: GH13441.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003701: arm:3R [9357746,9566163]
estimated-cyto:87F4-87F14: 04/10/2001
Plate: GH.134 row: D column: 5
High quality sequence stop: 593
POLYA-No.
Location/Qualifiers
1. .642
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="GH13441"
/sex="male and female"
/dev_stage="adult"
/lab_host="DHS - alpha"
/note="Organ: head; Vector: pOT2; Site 1: EcoRI; Site 2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."

ORIGIN
Query Match 65.4%; Score 18.6; DB 1; Length 642;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGGCAGAGAAACCG 26
||||| ||||||| ||||||| |||
Db 191 ATATGCTGAACGGCAGAGAAACCG 215

RESULT 30
CN882707 671 bp mRNA linear EST 04-JUN-2004
LOCUS 010812AASB00315GHT (AASB) Royal Gala 10 DAFB fruit Malus x
DEFINITION domestica cDNA clone AASB003156, mRNA sequence.
ACCESSION CN882707
VERSION CN882707.1 GI:48268949
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
1 (bases 1 to 671)
Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B.,
McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleave, A.
Sequencing Facility

```

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Fax: 00 64 09 815 4201
Email: est@hortresearch.co.nz.

FEATURES

source

1. 671
/organism="Malus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AASB003156"
/tissue_type="Young fruit"
/dev_stages="10 days after full bloom"
/clone_lib="(AASB) Royal Gala 10 DAFB fruit"
/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

ORIGIN

Query Match 66.4%; Score 18.6; DB 7; Length 671;
Best Local Similarity 84.0%; Pred. No. 1.1e+03;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 49 ATATCCTGAACGCGAGAGAGCTG 73

RESULT 31

CN879811

LOCUS

DEFINITION 010419AASB004412HT (AASA) Royal Gala 10 DAFB fruit Malus x domestica cDNA clone AASA004412, mRNA sequence.

ACCESSION

CN879811

VERSION

KEYWORDS

SOURCE

ORGANISM

Malus x domestica (cultivated apple)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosid1; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE

1 (bases 1 to 675)

AUTHORS

Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

HortResearch Apple EST Project

Unpublished (2004)

Contact: Gleave, A.

Sequencing Facility

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120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

Location/Qualifiers

1. 675

/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="AASA004412"

/tissue_type="Fruit"

/dev_stages="10 days after full bloom"

/clone_lib="(AASA) Royal Gala 10 DAFB fruit"

/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

Query Match 66.4%; Score 18.6; DB 7; Length 675;

Best Local Similarity 84.0%; Pred. No. 1.1e+03;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 60 ATATCCTGAACGCGAGAGAGCTG 84

RESULT 32

CN918097

LOCUS

DEFINITION 030203ABPB004660HT (ABPB) M9 root tips Malus x domestica cDNA clone ABPB004660, mRNA sequence.

ACCESSION

CN918097

VERSION

KEYWORDS

SOURCE

ORGANISM

Malus x domestica (cultivated apple)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosid1; Rosales; Rosaceae; Maloideae; Malus.

REFERENCE

1 (bases 1 to 683)

AUTHORS

Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

HortResearch Apple EST Project

Unpublished (2004)

Contact: Gleave, A.

Sequencing Facility

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120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200

Fax: 00 64 09 815 4201

Email: est@hortresearch.co.nz.

Location/Qualifiers

1. 683

/organism="Malus x domestica"

/mol_type="mRNA"

/db_xref="taxon:3750"

/clone="ABPB004660"

/tissue_type="Root tips (distal 1.5 cm)"

/clone_lib="(ABPB) M9 root tips"

/note="Vector: pBluescript SK(-); Library sequenced by
Genesis Research & Development"

Query Match 66.4%; Score 18.6; DB 7; Length 683;

Best Local Similarity 84.0%; Pred. No. 1.1e+03;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ATATGCTGAACGCGAGAGAACCG 26

Db 1 ATATCCTGAACGCGAGAGAGCTG 25

RESULT 33

AQ657387/c

LOCUS

DEFINITION Sheared DNA-2N16.TR Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-2N16, genomic survey sequence.

ACCESSION

AQ657387

VERSION

KEYWORDS

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 684)

AUTHORS

El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Garrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat

10.1 sheared DNA library

Unpublished (1999)

Other GSSs: Sheared DNA-2N16.TF

Contact: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: nelsayed@tigr.org
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/tdb/mdb/tbdb/>.
 Seq primer: M13-Reverse
 Class: shotgun.

FEATURES

source

1. .684
 /organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone_lib="Sheared DNA-2N16"
 /clone="Sheared DNA"

/notes="Vector: pUC18; Site 1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. in Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999)."

ORIGIN

Query Match 66.4%; Score 18.6; DB 8; Length 684;
 Best Local Similarity 84.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACC 25

||||| ||||| ||||| ||||| |||||
 Db 548 AATATCTGAAACGCCCAATTAACC 524

RESULT 34

CL527496

LOCUS

83k06rp42.f1 RPCI-42 Bos taurus genomic clone 83k06rp42, genomic survey sequence.

CL527496.1 GI:47120284

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 799)

Aycock,M.M., Najjar,F.Z., Gasbarre,L.C., Van Tassel,C.P.,

Sonstegard,T.S., Conner,E.E., Capuco,A.V. and Roe,B.A.

Bovine BAC End Sequences from RPCI-42 Library

Unpublished (2004)

Contact: Bruce A. Roe

Advanced Center for Genome Technology

University of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Class: BAC ends

High quality sequence start: 133

High quality sequence stop: 524.

Location/Qualifiers

1. .799

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="Holstein Bull"

/db_xref="taxon:9913"

/clone="83k06rp42"

/sex="male"

FEATURES

source

1. .799
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Holstein Bull"
 /db_xref="taxon:9913"
 /clone="83k06rp42"
 /sex="male"

ORIGIN

Query Match 66.4%; Score 18.6; DB 9; Length 799;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28

||||| ||||| ||||| ||||| |||||
 Db 63 AGTAGNCNGNAACGCGAGAAACACG 90

RESULT 35

CG016439

LOCUS

ZUAAG30TH_ZM_3_0_4_0_KB Zea mays genomic clone ZMWBPa0006E11, genomic survey sequence.

CG016439

VERSION

CG016439.1 GI:33888604

KEYWORDS

SOURCE

ORGANISM

Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 427)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,

Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,

Citek,R.W., Nunez,A., Robbins,D. and Lakey,N.

Consortium for Maize Genomics

Unpublished (2002)

Other GSSs: ZUAAG30TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: Sheared ends.

FEATURES

source

1. .427
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZM3_0_4_0_KB"
 /clone="ZMWBPa0006E11"
 /notes="Vector: pBCSK-; Site_1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN

Query Match 65.7%; Score 18.4; DB 9; Length 427;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28

||||| ||||| ||||| ||||| |||||
 Db 332 AATATGCTGCAACGCTAGAGAGGCGC 359

RESULT 36

AQ724090/c

LOCUS

AQ724090 456 bp DNA linear GSS 14-JUL-1999
 HS-5375_A2_H09_SP68 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=951 Col=18 Row=O, genomic survey sequence.

AQ724090

VERSION

AQ724090.1 GI:5483759

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Shvartsbeyn,A., Gebregorgis,B., Overton,L., Russell,D., Chen,D., Riggis,F., de Jong,P. and Fraser,C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished (1999)
 Other GSSs: CH230-39416-TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230
 (http://www.chori.org/bacpac/rat230.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/or ering information.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/rat/bac_end_intro.html
 Plate: 394 row: I column: 6
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source
 1. .582
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="Genomic DNA"
 /strain="BN/SeNHsd/MCW"
 /db_xref="taxon:10116"
 /clones="CH230-39416"
 /sex="Female"
 /cell_type="Brain"
 /clone_lib="CHORI-230 Segment 2"
 /note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
 CHORI-230 Rat (BN/SeNHsd/MCW) BAC library produced by
 Pieter de Jong"

ORIGIN

Query Match 65.7%; Score 18.4; DB 8; Length 582;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 DB 363 ACTCTGCTGATAGCAAGAGAAACCGCG 336

RESULT 39
 CB020289
 LOCUS
 DEFINITION
 CB020289.y1 Haemonchus contortus intestine SL2 TOPO v1 Haemonchus
 contortus cDNA 5' similar to TR:045912 O45812 T23G11.9 PROTEIN. [1]
 ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Haemonchus contortus
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.

REFERENCE
 AUTHORS
 1 (bases 1 to 655)
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
 Tagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Harwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson.R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. Oligo(dT)-SL2 PCR based
 library. cDNA PCR products of size >400 nucleotides containing SL2
 on the 5' end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning
 protocol. Intestine RNA was provided by Dr. Douglas Jasmier of
 Washington State University (djasmer@vetmed.wsu.edu).
 Seq primer: SL1 primer
 High quality sequence stop: 525.

FEATURES

source
 1. .655
 Location/Qualifiers
 /organism="Haemonchus contortus"
 /mol_type="mRNA"
 /db_xref="taxon:6289"
 /issue_type="intestine"
 /lab_host="DH10B"
 /clone_lib="Haemonchus contortus intestine SL2 TOPO v1"
 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI;
 Site 2: EcoRI; The library was constructed by Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. Oligo(dT)-SL2 PCR based library. cDNA PCR
 products of size >400 nucleotides containing SL2 on the 5'
 end and oligo(dT) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the Topo TA
 cloning protocol. Intestine RNA was provided by Dr.
 Douglas Jasmier of Washington State University
 (djasmer@vetmed.wsu.edu)."

ORIGIN

Query Match 65.7%; Score 18.4; DB 6; Length 655;
 Best Local Similarity 78.6%; Pred. No. 1.3e+03;
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
 DB 264 ATTTGCTGATGCGGAGAGAAACCGG 291

RESULT 40
 BH100535/c

LOCUS
 DEFINITION
 BH100535
 RPCI-24-333F21.TVB RPCI-24 Mus musculus genomic clone
 RPCI-24-333F21, genomic survey sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)

REFERENCE
 AUTHORS
 1 (bases 1 to 672)
 Zhong,S., Nierman,W., Malek,J., Shvartsbeyn,A., Gebregorgis,B.,
 Tsagayev,G., Geer,K., Krol,M., Shvartsbeyn,A., Akinret,B., Levins,M.,
 Russell,D., de Jong,P. and Fraser,C.M.
 Mouse BAC End Sequences from Library RPCI-24
 Unpublished (1999)
 Other GSSs: RPCI-24-333F21.TJ

COMMENT
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC
 library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org). Clones may be purchased from BACPAC
 Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
 page: http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html
 Plate: 333 row: F column: 21
 Seq primer: T7

Class: BAC ends.
Location/Qualifiers
1. 672
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-333F21"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

ORIGIN
Query Match 65.7%; Score 18.4; DB 8; Length 672;
Best Local Similarity 78.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 374 ACTTTGCTGAAAGCGCAAGAGAAAGCGCG 347
|||||

RESULT 41
CA112278 675 bp mRNA linear EST 23-SEP-2003
LOCUS SCEPLB1043H05.9 LB1 Saccharum officinarum cDNA clone SCEPLB1043H05
DEFINITION 5' mRNA sequence.
ACCESSION CA112278.1 GI:34965585
VERSION
KEYWORDS
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE
1 (bases 1 to 675)
Vettore A.L., da Silva F.R., Kemper E.L. and Arruda P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>
Seq primer: 043 row: H column: 05
Plate: 043 row: H column: 05
Location/Qualifiers
1. 675
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCEPLB1043H05"
/lab_host="DH10B"
/clone_lib="LB1"
/note="Organ: Lateral buds from field grown adult plants; Vector: pSPori1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [lateral buds from field grown adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN
Query Match 65.7%; Score 18.4; DB 6; Length 675;
Best Local Similarity 78.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 581 ATTATGCTGAACCTCGAGGAACTGGG 608
|||||

RESULT 42
BH929269/c 695 bp DNA linear GSS 01-OCT-2002
LOCUS od18f08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION sequence.
ACCESSION BH929269
VERSION BH929269.1 GI:23409335
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 695)
Delehaunty K., Fewell G., Fulton L., McCombie W.R., Miner T., Nash W., Rabinowicz P.D. and Wilson R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: od18f row: f column: 08
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 32
High quality sequence stop: 513.
Location/Qualifiers
1. 695
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

FEATURES
source
1. 695
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
Query Match 65.7%; Score 18.4; DB 8; Length 695;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATATGCTGAACGCGAGAGAAACCGCG 28
|||||
Db 162 AAAATGCGGACGAGAGAGAAACCGCG 135
|||||

RESULT 43
BH549312/c 697 bp DNA linear GSS 14-DEC-2001
LOCUS BOHEP93TR BOHE Brassica oleracea genomic clone BOHEP93, genomic survey sequence.
DEFINITION BH549312
ACCESSION BH549312
VERSION BH549312.1 GI:17801092
KEYWORDS GSS.

```

SOURCE
ORGANISM
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 697)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOHEP93TF
Contact: Chris Town
TIGR Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES
source
Location/Qualifiers
1..697
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TOL000H3"
/db_xref="taxon:3712"
/clone="BOHEP93"
/clone_lib="BOHE"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
Query Match 65.7%; Score 18.4; DB 9; Length 697;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 588 AAAATGCCAACACGCGACGAGAACCGCG 561

RESULT 44
CK326303 743 bp mRNA linear EST 17-DEC-2003
LOCUS
DEFINITION
Hd mx23_03A06_T7 Hypsibius dujardini mixed stage 5' capped (fraction
3) Hypsibius dujardini cDNA clone Hd mx23_03A06 5' similar to
Q99JR7 (Q99JR7) RIKEN cDNA 2610012022 gene, mRNA sequence.
CK326303
CK326303.1 GI:39999894
ACCESSION
EST.
KEYWORDS
SOURCE
Hypsibius dujardini
Hypsibius dujardini
Eukaryota; Metazoa; Tardigrada; Eutardigrada; Apochela;
Hypsibiidae; Hypsibius.
REFERENCE
1 (bases 1 to 743)
Daub, J., Thomas, F., Aboobaker, A. and Blaxter, M.L.
A survey of genes expressed in the tardigrade Hypsibius dujardini
Unpublished (2003)
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JT, UK.
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
PCR Primers
FORWARD: M13R
BACKWARD: M13L
Plate: 03 row: A column: 06
Seq primer: T7 (TAATACGACTCACTATAGGG)
High quality sequence stop: 481.
FEATURES
source
Location/Qualifiers
1..743
/organism="Hypsibius dujardini"
/mol_type="mRNA"
/db_xref="taxon:232323"
/clone="Hd mx23_03A06"
/sex="parthenogenic"
/tissue_type="whole body"
/dev_stage="mixed (adult and juvenile)"
/clone_lib="Hypsibius dujardini mixed stage 5' capped
(fraction 3)"
/note="Vector: pSPORT1; Site 1: Sal I (5' end); Site 2: Not
I (3' end); Tardigrades (also know as water bears) are
small free living animals inhabiting marine, fresh water
and water film habitats. Hypsibius dujardini is a
freshwater species maintained in lab culture (source
strain Sciento 2151). The library was prepared from adults
and juveniles and was constructed in pSPORT1 vector
(Superscript, Invitrogen) using GeneRacer (Invitrogen)
purified 5' capped mRNA by Jennifer Daub, University of
Edinburgh. Sequencing was performed by Frances Thomas,
University of Edinburgh."

ORIGIN
Query Match 65.7%; Score 18.4; DB 7; Length 743;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATATGCTGAACGCGAGAGAAACCGCG 28
||||| ||||| ||||| ||||| |||||
Db 230 AAAATGCCGAATCCAAGCGAACCAGCG 257

RESULT 45
BE615972 750 bp mRNA linear EST 24-AUG-2000
LOCUS
DEFINITION
601279483F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3611516 5',
mRNA sequence.
BE615972
BE615972.1 GI:9897658
ACCESSION
EST.
KEYWORDS
SOURCE
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 750)
NIH-MGC http://mgc.nci.nih.gov/.
NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM269 row: e column: 21
High quality sequence stop: 551.
FEATURES
source
Location/Qualifiers
1..750
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3611516"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_39"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GCCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA

```


AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1144 row: e column: 08
High quality sequence start: 174
High quality sequence stop: 509.
Location/Qualifiers
1. .790
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294639"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NTH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccatattgcc-3' as follows: 5' and 3' adaptors were used in cloning and 3' adaptor sequence: 5'-ATTCTGAGGCGGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 65.7%; Score 18.4; DB 2; Length 790;
Best Local Similarity 95.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 ATGCTGAACCGGAGAGAAA 23
|||||
Db 270 ATGCTGAACCGGAGAGAAA 289
|||||
RESULT 49
Bi753870
LOCUS Bi753870.1 GI:15745448
DEFINITION Bi753870 792 bp mRNA linear EST 25-SEP-2001
mRNA sequence.
ACCESSION Bi753870
VERSION Bi753870.1 GI:15745448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 792)
NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM11495 row: d column: 16
High quality sequence stop: 761.
Location/Qualifiers
FEATURES
source

NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1144 row: e column: 08
High quality sequence start: 174
High quality sequence stop: 509.
Location/Qualifiers
1. .790
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294639"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NTH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccatattgcc-3' as follows: 5' and 3' adaptors were used in cloning and 3' adaptor sequence: 5'-ATTCTGAGGCGGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 65.7%; Score 18.4; DB 2; Length 790;
Best Local Similarity 95.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 ATGCTGAACCGGAGAGAAA 23
|||||
Db 270 ATGCTGAACCGGAGAGAAA 289
|||||
RESULT 49
Bi753870
LOCUS Bi753870.1 GI:15745448
DEFINITION Bi753870 792 bp mRNA linear EST 25-SEP-2001
mRNA sequence.
ACCESSION Bi753870
VERSION Bi753870.1 GI:15745448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 792)
NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM11495 row: d column: 16
High quality sequence stop: 761.
Location/Qualifiers
FEATURES
source

NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1144 row: e column: 08
High quality sequence start: 174
High quality sequence stop: 509.
Location/Qualifiers
1. .790
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294639"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NTH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccatattgcc-3' as follows: 5' and 3' adaptors were used in cloning and 3' adaptor sequence: 5'-ATTCTGAGGCGGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 65.7%; Score 18.4; DB 2; Length 790;
Best Local Similarity 95.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 ATGCTGAACCGGAGAGAAA 23
|||||
Db 270 ATGCTGAACCGGAGAGAAA 289
|||||
RESULT 49
Bi753870
LOCUS Bi753870.1 GI:15745448
DEFINITION Bi753870 792 bp mRNA linear EST 25-SEP-2001
mRNA sequence.
ACCESSION Bi753870
VERSION Bi753870.1 GI:15745448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 792)
NTH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM11495 row: d column: 16
High quality sequence stop: 761.
Location/Qualifiers
FEATURES
source

NIH-MGC <http://mgc.nci.nih.gov/>;
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1144 row: e column: 08
High quality sequence start: 174
High quality sequence stop: 509.
Location/Qualifiers
1. .790
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4294639"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NTH MGC 83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgctcgcc); Site_2: SfiI (ggccatattgcc-3' as follows: 5' and 3' adaptors were used in cloning and 3' adaptor sequence: 5'-ATTCTGAGGCGGAGCGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN
Query Match 65.7%; Score 18.4; DB 4; Length 792;
Best Local Similarity 78.6%; Pred. No. 1.4e+03;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AATATGCTGAACCGGAGAGAACCCGCG 28
|||||
Db 446 AAGATGCTGAATGGGGAGAGCCCGTG 473
|||||
RESULT 50
Bi753870/c
LOCUS Bi753870.1 GI:13109595
DEFINITION Bi753870 824 bp mRNA linear EST 22-OCT-2001
HVSMEC0020G05f Hordeum vulgare seedling shoot EST library
HVCdNA0003 (Etiolated and unstressed) Hordeum vulgare subsp.
vulgare cDNA clone HVSMEC0020G05f, mRNA sequence.
ACCESSION Bi753870.1 GI:13109595
VERSION Bi753870.1 GI:13109595
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 824)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
On Dec 18, 2000 this sequence version replaced gi:11884347.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: wing@clemson.edu
Total hg bases = 279
Seq primer: AATTAACTCACTAAAGGG
High quality sequence stop: 535.
Location/Qualifiers
1. .824
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSMEC0020G05f"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCdNA0003 (Etiolated and unstressed)"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
source

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